

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2005, 11:02:02 ; Search time 175 Seconds
(without alignments)
553.046 Million cell updates/sec

Title: US-09-823-077C-7

Perfect score: 1085
Sequence: 1 DSWMTSLNFIAGTTCVCLGON.....GPSLYSLSPSPPLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1060	97.7	226	2	Q6XG88 hepatitis b
2	1060	97.7	226	2	Q8BAN9 hepatitis b
3	1060	97.7	281	2	Q6XG39 hepatitis b
4	1060	97.7	389	2	Q6XG10 hepatitis b
5	1054	97.1	222	2	Q9DI79 hepatitis b
6	1054	97.1	222	2	Q9DI75 hepatitis b
7	1054	97.1	226	2	Q69601 hepatitis b
8	1054	97.1	226	2	Q8BAN3 hepatitis b
9	1054	97.1	226	2	Q8BAN5 hepatitis b
10	1054	97.1	226	2	Q8BAN8 hepatitis b
11	1054	97.1	226	2	Q9PX80 hepatitis b
12	1054	97.1	281	2	Q41762 hepatitis b
13	1054	97.1	281	2	Q6XG10 hepatitis b
14	1054	97.1	281	2	Q9J136 hepatitis b
15	1054	97.1	281	2	Q9J137 hepatitis b
16	1054	97.1	281	2	Q9PW75 hepatitis b
17	1054	97.1	337	2	Q70BB2 hepatitis b
18	1054	97.1	389	2	Q68843 hepatitis b
19	1054	97.1	389	2	Q67871 hepatitis b
20	1054	97.1	389	2	Q67879 hepatitis b
21	1054	97.1	389	2	Q6XG11 hepatitis b
22	1054	97.1	389	2	Q7T4U0 hepatitis b
23	1054	97.1	389	2	Q7T4U6 hepatitis b
24	1054	97.1	389	2	Q9PW6 hepatitis b
25	1054	97.1	389	2	Q9WJ4 hepatitis b
26	1054	97.1	400	2	Q80J12 hepatitis b
27	1051	96.9	226	2	Q8BAN9 hepatitis b
28	1050	96.8	222	2	Q9DI79 hepatitis b
29	1050	96.8	226	2	Q8AZ60 hepatitis b
30	1050	96.8	281	2	Q41750 hepatitis b
31	1050	96.8	281	2	Q41751 hepatitis b

32	1050	96.8	281	2	Q8AY12 hepatitis b
33	1050	96.8	370	2	Q8AZ54 hepatitis b
34	1050	96.8	389	2	Q7T4V2 hepatitis b
35	1050	96.8	389	2	Q9IF39 hepatitis b
36	1049	96.7	226	2	Q67910 hepatitis b
37	1049	96.7	226	2	Q6XGK3 hepatitis b
38	1049	96.7	226	2	Q8BAN5 hepatitis b
39	1049	96.7	226	2	Q9Q3D5 hepatitis b
40	1049	96.7	226	2	Q9QAF5 hepatitis b
41	1049	96.7	281	2	Q67915 hepatitis b
42	1049	96.7	281	2	Q6XGK4 hepatitis b
43	1049	96.7	281	2	Q9QAF1 hepatitis b
44	1049	96.7	389	2	Q67886 hepatitis b
45	1049	96.7	389	2	Q67914 hepatitis b

ALIGNMENTS

RESULT 1

ID	Q6XG88	PRELIMINARY;	PRT;	226 AA.
AC	Q6XG88			
DT	05-JUL-2004 (Tremblrel. 27, Created)			
DT	05-JUL-2004 (Tremblrel. 27, Last sequence update)			
DT	05-JUL-2004 (Tremblrel. 27, Last annotation update)			
DS	S protein.			
OS	Hepatitis B virus.			
OC	Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.			
NCBI_TaxID=10407;				
RM	[1]			
RP	SEQUENCE FROM N.A.			
RX	Pubmed=1510537; DOI=10.1099/vir.0.19749-0;			
RA	Kimbl G.C., Kramvis A., Kew M.C.;			
RT	"Distinctive sequence characteristics of subgenotype A1 isolates of			
RT	hepatitis B virus from South Africa."			
RL	J. Gen. Virol. 85:1211-1220 (2004).			
DR	EMBL; AY233296; AAP79871.1; -			
DR	GO; GO:0016032; P:Viral life cycle; IEA.			
DR	InterPro; IPR000349; Hepvir_surfg.			
DR	Pfam; PF00695; VMSA; 1.			
KW	Antigen.			
SO	SEQUENCE	226 AA;	25361 MW;	228209BESD7D204D CRC64;
Query Match 97.7%; Score 1060; DB 2; Length 226;				
Best Local Similarity 97.4%; Pred. No. 2e-82; Mismatches 3; Indels 0; Gaps 0;				
Matches 184; Conservative 2; Mismatches 3; Indels 0; Gaps 0;				
QY	1 DSWMTSLNFIAGTTCVCLGONSQSPTSNHSPSCPTCPGRMCLRRPIIFLFIILLCLI 60			
DB	33 DSWMTSLNFIAGTTCVCLGONSQSPTSNHSPSCPTCPGRMCLRRPIIFLFIILLCLI 92			
QY	61 FLVLLDYOGILPVCPILPSSSTSGQCRCTTPAGGTMYBSCCTCKPDGCTCPI 120			
DB	93 FLVLLDYOGILPVCPILPSSSTSGQCRCTTPAGGTMYBSCCTCKPDGCTCPI 152			
QY	121 PSSWAFKYLWENASAFWSLSLVPVQWFGSLPVTMLSVIMMYWGLSLSLSPF 180			
DB	153 PSSWAFKYLWENASAFWSLSLVPVQWFGSLPVTMLSVIMMYWGLSLSLSPF 212			
QY	181 SPLPIFFC 189			
DB	213 SPLPIFFC 221			
RESULT 2				
QY	Q8BAN9	PRELIMINARY;	PRT;	226 AA.
AC	Q8BAN9			
DT	01-MAR-2003 (Tremblrel. 23, Created)			
DT	01-MAR-2003 (Tremblrel. 23, Last sequence update)			
DT	01-JUL-2003 (Tremblrel. 24, Last annotation update)			
DS	Surface antigen.			

```
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Bowden R.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Basant A.A., Bowden R.J., Butterworth L.-A., Cooksey G.,
  Locarnini S., Garman W.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY122559; AAM82961.1;
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surtag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 226 AA; 25361 MW; 228209P95608229D CRC64;

Query Match 97.7%; Score 1060; DB 2; Length 226;
Best Local Similarity 97.4%; Pred. No. 2e-82; Mismatches 3; Indels 0; Gaps 0;
Matches 184; Conservative 2;

QY 1 DSWMTSLNFIAGTTVCIGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLLILCL 60
DB 33 DSWMTSLNFIAGTTVCIGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLLILCL 92
QY 61 FLVLVDYQGLVPCPLIPSSSTTSKQOCRTCTTPAAGTSMYPSCCCTKPSDGNCTCIP 120
DB 93 FLVLVDYQGLVPCPLIPSSSTTSKQOCRTCTTPAAGTSMYPSCCCTKPSDGNCTCIP 152
QY 121 PSSMAFGKTYMEWASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLYSLISPF 180
DB 153 PSSMAFGKTYMEWASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLYSLISPF 212
QY 181 SPLPIFFC 189
DB 213 SPLPIFFC 221

RESULT 3
Q6XG9 PRELIMINARY; PRT; 281 AA.
AC 06XG9;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Middle S protein.
DE Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimb G.C., Kramvis A., Kew M.C.;
RL "Distinctive sequence characteristics of subgenotype A1 isolates of
  hepatitis B virus from South Africa.";
RT J. Gen. Virol. 85:1211-1220(2004).
DR EMBL; AY233296; AAP79872.1;
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surtag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 281 AA; 31206 MW; B95FEC6AD353604F CRC64;

Query Match 97.7%; Score 1060; DB 2; Length 281;
Best Local Similarity 97.4%; Pred. No. 2.4e-82; Mismatches 3; Indels 0; Gaps 0;
Matches 184; Conservative 2;

QY 1 DSWMTSLNFIAGTTVCIGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLLILCL 60
DB 88 DSWMTSLNFIAGTTVCIGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLLILCL 147
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QY 61 FLVLVDYQGLVPCPLIPSSSTTSKQOCRTCTTPAAGTSMYPSCCCTKPSDGNCTCIP 120
DB 148 FLVLVDYQGLVPCPLIPSSSTTSKQOCRTCTTPAAGTSMYPSCCCTKPSDGNCTCIP 207
QY 121 PSSMAFGKTYMEWASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLYSLISPF 180
DB 208 PSSMAFGKTYMEWASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLYSLISPF 267
QY 181 SPLPIFFC 189
DB 268 SPLPIFFC 276

RESULT 4
Q6XG9 PRELIMINARY; PRT; 389 AA.
AC 06XG9;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Large S protein.
DE Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Kimb G.C., Kramvis A., Kew M.C.;
RL "Distinctive sequence characteristics of subgenotype A1 isolates of
  hepatitis B virus from South Africa.";
RT J. Gen. Virol. 85:1211-1220(2004).
DR EMBL; AY233296; AAP79872.1;
DR GO; GO:0016032; P: viral life cycle; IEA.
DR InterPro; IPR000349; Hepvir_surtag.
DR Pfam; PF00695; VMSA; 1.
KW Antigen.
SQ SEQUENCE 389 AA; 42691 MW; CEE26773DFC603F2 CRC64;

Query Match 97.7%; Score 1060; DB 2; Length 389;
Best Local Similarity 97.4%; Pred. No. 3.3e-82; Mismatches 3; Indels 0; Gaps 0;
Matches 184; Conservative 2;

QY 1 DSWMTSLNFIAGTTVCIGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLLILCL 60
DB 196 DSWMTSLNFIAGTTVCIGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLLILCL 255
QY 61 FLVLVDYQGLVPCPLIPSSSTTSKQOCRTCTTPAAGTSMYPSCCCTKPSDGNCTCIP 120
DB 256 FLVLVDYQGLVPCPLIPSSSTTSKQOCRTCTTPAAGTSMYPSCCCTKPSDGNCTCIP 315
QY 121 PSSMAFGKTYMEWASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLYSLISPF 180
DB 316 PSSMAFGKTYMEWASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLYSLISPF 375
QY 181 SPLPIFFC 189
DB 376 SPLPIFFC 384

RESULT 5
Q9DIT9 PRELIMINARY; PRT; 222 AA.
AC 09DIT9;
DT 01-MAR-2001 (TEMBLrel. 16, Created)
DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update)
DE Surface antigen (Fragment).
OC Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OX NCBI_TaxID=10407;
RN [1]
RP SEQUENCE FROM N.A.
RA Liu H.F.;
```

RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ297881; CAC0278.1; -; HepViral life cycle; IEA.
 DR GO: 0016032; P: viral life cycle; IEA.
 DR InterPro: IPR000349; HepViral_surfactant.
 DR Pfam: PF00695; VMSA; 1.
 DR Antigen.
 KM Antigen.

FT NON TER 222 222
 SEQUENCE 222 AA; 24825 MW; 9D65834D72D4FBD3 CRC64;

Query Match 97.1%; Score 1054; DB 2; Length 222;
 Best Local Similarity 96.8%; Pred. No. 6.4e-82;
 Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSWMTSLNLFAGTTCVCGQNSQSPNSHSPSCPTCGYRMCLRRRIIFILLICLI 60
 DB 33 DSWMTSLNLFAGTTCVCGQNSQSPNSHSPSCPTCGYRMCLRRRIIFILLICLI 92
 QY 61 FLVLLDYQGLPVCPLIPGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
 DB 93 FLVLLDYQGLPVCPLIPGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDGNCTCIP 152
 QY 121 PSSNAFGKYLWEMASARPSWLSLVFVQMFVGLSPTVWLSVIMMMYWGSPSLYSILSP 180
 DB 153 PSSNAFGKYLWEMASARPSWLSLVFVQMFVGLSPTVWLSVIMMMYWGSPSLYSILSP 212
 QY 181 SPLLPFFC 189
 DB 213 LPLLPFFC 221

RESULT 6
 Q9DIV5 PRELIMINARY; PRT; 222 AA.

AC Q9DIV5; 01-MAR-2001 (TREMREL. 16, Created)
 DT 01-MAR-2001 (TREMREL. 16, Last sequence update)
 DT 01-JUN-2003 (TREMREL. 24, Last annotation update)
 DE Surface antigen (fragment).
 OS Hepatitis B virus.
 OC Viruses; Retroviridae; Orthohepadnavirus.
 CX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu H.P.;
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ297885; CAC0262.1; -;
 DR GO: 0016032; P: viral life cycle; IEA.
 DR InterPro: IPR000349; HepViral_surfactant.
 DR Pfam: PF00695; VMSA; 1.
 DR Antigen.
 KM Antigen.
 FT NON TER 222 222
 SEQUENCE 222 AA; 24825 MW; 9D65834D72D4FBD3 CRC64;

Query Match 97.1%; Score 1054; DB 2; Length 222;
 Best Local Similarity 96.8%; Pred. No. 6.4e-82;
 Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSWMTSLNLFAGTTCVCGQNSQSPNSHSPSCPTCGYRMCLRRRIIFILLICLI 60
 DB 33 DSWMTSLNLFAGTTCVCGQNSQSPNSHSPSCPTCGYRMCLRRRIIFILLICLI 92
 QY 61 FLVLLDYQGLPVCPLIPGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
 DB 93 FLVLLDYQGLPVCPLIPGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDGNCTCIP 152
 QY 121 PSSNAFGKYLWEMASARPSWLSLVFVQMFVGLSPTVWLSVIMMMYWGSPSLYSILSP 180
 DB 153 PSSNAFGKYLWEMASARPSWLSLVFVQMFVGLSPTVWLSVIMMMYWGSPSLYSILSP 212
 QY 181 SPLLPFFC 189
 DB 213 LPLLPFFC 221

RESULT 7

Q69601 PRELIMINARY; PRT; 226 AA.
 AC Q69601; 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
 DE S gene subtype aYW2 protein.
 GN Name=S gene subtype aYW2;
 OS Hepatitis B virus.
 OC Viruses; Retroviridae; Orthohepadnavirus.
 CX NCBI_TaxID=10407;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Norde H., Hammes B., Lefdal S., Courrouc A.M., Magnus L.O.;
 RX MEDLINE=92268879; PubMed=1588323;
 RT "Comparison of the amino acid sequences of nine different serotypes of
 RT Hepatitis B surface antigen and genomic classification of the
 RT corresponding hepatitis B virus strains.";
 RT J. Gen. Virol. 73:1201-1208 (1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Norde H.M.L.;
 RC STRAIN=genotype D;
 RL EMBL: X75662; CAA53349.1; -;

DR EMBL: X75662; CAA53349.1; -;
 DR PIR: J01571; J01571.
 DR PIR: J01572; J01572.
 DR PIR: J02063; J02063.
 DR PIR: J02066; J02066.
 DR PIR: J02067; J02067.
 DR PIR: J02068; J02068.
 DR PIR: J02069; J02069.
 DR PIR: J02070; J02070.
 DR PIR: J02072; J02072.
 DR PIR: J02076; J02076.
 DR PIR: J02077; J02077.
 DR PIR: J02079; J02079.
 DR PIR: J02081; J02081.
 DR PIR: J02083; J02083.
 DR GO: 0016032; P: viral life cycle; IEA.
 DR InterPro: IPR000349; HepViral_surfactant.
 DR Pfam: PF00695; VMSA; 1.
 DR Antigen.
 KM Antigen.
 FT NON TER 226 226
 SEQUENCE 226 AA; 25460 MW; C68303545C6838B6 CRC64;

Query Match 97.1%; Score 1054; DB 2; Length 226;
 Best Local Similarity 96.8%; Pred. No. 6.5e-82;
 Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSWMTSLNLFAGTTCVCGQNSQSPNSHSPSCPTCGYRMCLRRRIIFILLICLI 60
 DB 33 DSWMTSLNLFAGTTCVCGQNSQSPNSHSPSCPTCGYRMCLRRRIIFILLICLI 92
 QY 61 FLVLLDYQGLPVCPLIPGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
 DB 93 FLVLLDYQGLPVCPLIPGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDGNCTCIP 152
 QY 121 PSSNAFGKYLWEMASARPSWLSLVFVQMFVGLSPTVWLSVIMMMYWGSPSLYSILSP 180
 DB 153 PSSNAFGKYLWEMASARPSWLSLVFVQMFVGLSPTVWLSVIMMMYWGSPSLYSILSP 212
 QY 181 SPLLPFFC 189
 DB 213 LPLLPFFC 221

RESULT 8

Q8BAM3 PRELIMINARY; PRT; 226 AA.
 ID Q8BAM3
 AC Q8BAM3;

```
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DS Surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OK NCBI_TaxId=10407;
RN
RP SEQUENCE FROM N.A.
RA Bowden R.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN
[2]
RP SEQUENCE FROM N.A.
RA Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
  Locarnini S., Carman W.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY122567; AAM82977.1; -
DR GO: GO:0016032; P: viral life cycle; IEA.
DR InterPro: IPR000349; Hepvir_surtag.
DR Pfam: PF00695; VMSA; 1.
DR Antigen.
SQ SEQUENCE 226 AA; 25359 MW; 9C60B38B9DFDC928 CRC64;

Query Match
Best Local Similarity 97.1%; Score 1054; DB 2; Length 226;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSWTSLNIFLGGTTVCLIGONSQSPSTNSHPTSCPTCPGGRMCLRRFIIFLLILCLT 60
   |||||
DB 33 DSWTSLNIFLGGTTVCLIGONSQSPSTNSHPTSCPTCPGGRMCLRRFIIFLLILCLT 92
   |||||

QY 61 FLVLVDYQGLFVPCPLIPSSSTTSKGQCRCTCTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
   |||||
DB 93 FLVLVDYQGLFVPCPLIPSSSTTSKGQCRCTCTTPAOGTSMYPSCCCTKPSDGNCTCIP 152
   |||||

QY 121 PSSMARGKYLMEWASARFWSLSLVPFVQVFGLSPTVMSVIMMMWYMGPSLYSILSPF 180
   |||||
DB 153 PSSMARGKYLMEWASARFWSLSLVPFVQVFGLSPTVMSVIMMMWYMGPSLYSILSPF 212
   |||||

QY 181 SPLLPPIFFC 189
   |||||
DB 213 SPLLPPIFFC 221
   |||||

RESULT 9
OBBAP8
ID OBBAP8 PRELIMINARY; PRT; 226 AA.
AC OBBAP8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DS Surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OK NCBI_TaxId=10407;
RN
RP SEQUENCE FROM N.A.
RA Bowden R.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN
[2]
RP SEQUENCE FROM N.A.
RA Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
  Locarnini S., Carman W.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY122561; AAM82965.1; -
DR GO: GO:0016032; P: viral life cycle; IEA.
DR InterPro: IPR000349; Hepvir_surtag.
DR Pfam: PF00695; VMSA; 1.
DR Antigen.
SQ SEQUENCE 226 AA; 25387 MW; B4D69BF2A626A43 CRC64;

Query Match
Best Local Similarity 97.1%; Score 1054; DB 2; Length 226;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
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```
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSWTSLNIFLGGTTVCLIGONSQSPSTNSHPTSCPTCPGGRMCLRRFIIFLLILCLT 60
   |||||
DB 33 DSWTSLNIFLGGTTVCLIGONSQSPSTNSHPTSCPTCPGGRMCLRRFIIFLLILCLT 92
   |||||

QY 61 FLVLVDYQGLFVPCPLIPSSSTTSKGQCRCTCTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
   |||||
DB 93 FLVLVDYQGLFVPCPLIPSSSTTSKGQCRCTCTTPAOGTSMYPSCCCTKPSDGNCTCIP 152
   |||||

QY 121 PSSMARGKYLMEWASARFWSLSLVPFVQVFGLSPTVMSVIMMMWYMGPSLYSILSPF 180
   |||||
DB 153 PSSMARGKYLMEWASARFWSLSLVPFVQVFGLSPTVMSVIMMMWYMGPSLYSILSPF 212
   |||||

QY 181 SPLLPPIFFC 189
   |||||
DB 213 SPLLPPIFFC 221
   |||||

RESULT 10
OBBAP8
ID OBBAP8 PRELIMINARY; PRT; 226 AA.
AC OBBAP8;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DS Surface antigen.
OS Hepatitis B virus.
OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
OK NCBI_TaxId=10407;
RN
RP SEQUENCE FROM N.A.
RA Bowden R.J.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN
[2]
RP SEQUENCE FROM N.A.
RA Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
  Locarnini S., Carman W.F.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY122552; AAM82947.1; -
DR GO: GO:0016032; P: viral life cycle; IEA.
DR InterPro: IPR000349; Hepvir_surtag.
DR Pfam: PF00695; VMSA; 1.
DR Antigen.
SQ SEQUENCE 226 AA; 25374 MW; 465BEB30B0EB1D CRC64;

Query Match
Best Local Similarity 97.1%; Score 1054; DB 2; Length 226;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DSWTSLNIFLGGTTVCLIGONSQSPSTNSHPTSCPTCPGGRMCLRRFIIFLLILCLT 60
   |||||
DB 33 DSWTSLNIFLGGTTVCLIGONSQSPSTNSHPTSCPTCPGGRMCLRRFIIFLLILCLT 92
   |||||

QY 61 FLVLVDYQGLFVPCPLIPSSSTTSKGQCRCTCTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
   |||||
DB 93 FLVLVDYQGLFVPCPLIPSSSTTSKGQCRCTCTTPAOGTSMYPSCCCTKPSDGNCTCIP 152
   |||||

QY 121 PSSMARGKYLMEWASARFWSLSLVPFVQVFGLSPTVMSVIMMMWYMGPSLYSILSPF 180
   |||||
DB 153 PSSMARGKYLMEWASARFWSLSLVPFVQVFGLSPTVMSVIMMMWYMGPSLYSILSPF 212
   |||||

QY 181 SPLLPPIFFC 189
   |||||
DB 213 SPLLPPIFFC 221
   |||||

RESULT 11
OBBAP8
ID OBBAP8 PRELIMINARY; PRT; 226 AA.
AC OBBAP8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
```

DT 05-JUL-2004 (TrEMBLrel. 27, last annotation update)
 DE S protein (Major surface antigen).
 OC Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 NCBI_TaxID=10407;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20109034; PubMed=10640544;
 RA Hannon C., Horal P., Lindh M.;
 RT "Long-term mutation rates in the hepatitis B virus genome";
 J. Gen. Virol. 81:75-83(2000).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=438;
 RX MEDLINE=20345625; PubMed=10884611; DOI=10.1016/S1286-4579(00)00365-8;
 RA Barchani-Chabchoub I., Gargouri A., Mokdad-Gargouri R.;
 RT "Genotyping of Tunisian hepatitis B virus isolates based on the
 sequencing of preS2 and S regions";
 J. Microbes Infect. 2:607-612(2000).
 RN (3)
 RP SEQUENCE FROM N.A.
 RA Bowden R.J.;
 RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN (4)
 RP SEQUENCE FROM N.A.
 RA Basuni A.A., Bowden R.J., Butterworth L.-A., Cooksley G.,
 Locantini S., Carman W.F.;
 RT Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 RN (5)
 RP SEQUENCE FROM N.A.
 RX PubMed=15105537; DOI=10.1099/vir.0.19749-0;
 RA Kimbri G.C., Krawlis A., Kew M.C.;
 RT "Distinctive sequence characteristics of subgenotype A1 isolates of
 hepatitis B virus from South Africa";
 J. Gen. Virol. 85:1211-1220(2004).
 RN EMBL; AF121241; AAF24676.1; -
 DR EMBL; AF229159; AAF40187.1; -
 DR EMBL; AY122553; AAM82949.1; -
 DR EMBL; AY122554; AAM82951.1; -
 DR EMBL; AY122557; AAM82957.1; -
 DR EMBL; AY122558; AAM82959.1; -
 DR EMBL; AY122558; AAM82979.1; -
 DR EMBL; AY122589; AAM83021.1; -
 DR EMBL; AY233293; AAF79850.1; -
 DR EMBL; AP212440; AAF24669.1; -
 DR PIR; J01572; J01572.
 DR PIR; J02063; J02063.
 DR PIR; J02066; J02066.
 DR PIR; J02067; J02067.
 DR PIR; J02068; J02068.
 DR PIR; J02069; J02069.
 DR PIR; J02070; J02070.
 DR PIR; J02072; J02072.
 DR PIR; J02076; J02076.
 DR PIR; J02077; J02077.
 DR PIR; J02079; J02079.
 DR PIR; J02081; J02081.
 DR PIR; J02083; J02083.
 DR PIR; J02091; J02091.
 DR PIR; J02092; J02092.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surtag.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 226 AA; 25387 MW; 22820985D65834D CRC64;
 Query Match 97.1%; Score 1054; DB 2; Length 226;
 Best Local Similarity 96.8%; Pred. No. 6.5e-82;
 Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DSWMTSLNPLGTTVCLGNSQSPSTNSPTSCPTCPGYRMWCLARRPIIFILLCLII 60
 DB 33 DSWMTSLNPLGTTVCLGNSQSPSTNSPTSCPTCPGYRMWCLARRPIIFILLCLII 92

QY 61 FLVLYLDYQGLPVCPLIPGSSSTTSKQCRCTTPAAGTSMYPSGCCCTKBDGCTCPIPI 120
 DB 93 FLVLYLDYQGLPVCPLIPGSSSTTSKQCRCTTPAAGTSMYPSGCCCTKBDGCTCPIPI 152
 QY 121 PSSWAFGKFLMEWASARFSLVLPVQWFGVLSPTVMVIMMMYMGSLYSLSLSPF 180
 DB 153 PSSWAFGKFLMEWASARFSLVLPVQWFGVLSPTVMVIMMMYMGSLYSLSLSPF 212
 QY 181 SPLLPFFC 189
 DB 213 SPLLPFFC 221
 RESULT 12
 ID 041762 PRELIMINARY; PRT; 281 AA.
 AC 041762
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE Middle S protein.
 GN Name=preS2/S;
 OS Hepatitis B virus.
 OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.
 OC NCBI_TaxID=10407;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97368435; PubMed=9225049;
 RA Boyer S., van Staden L., Kew M.C., Sim J.G.;
 RT "A unique segment of the hepatitis B virus group A genotype identified
 in isolates from South Africa";
 J. Gen. Virol. 78:1719-1729(1997).
 RN EMBL; U87851; AAC58030.1; -
 DR PIR; J01572; J01572.
 DR PIR; J02063; J02063.
 DR PIR; J02066; J02066.
 DR PIR; J02067; J02067.
 DR PIR; J02068; J02068.
 DR PIR; J02069; J02069.
 DR PIR; J02070; J02070.
 DR PIR; J02072; J02072.
 DR PIR; J02076; J02076.
 DR PIR; J02077; J02077.
 DR PIR; J02079; J02079.
 DR PIR; J02081; J02081.
 DR PIR; J02083; J02083.
 DR PIR; J02091; J02091.
 DR PIR; J02092; J02092.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surtag.
 DR Pfam; PF00695; VMSA; 1.
 KW Antigen.
 SQ SEQUENCE 281 AA; 31338 MW; 74ADAD08B3491BC9 CRC64;
 Query Match 97.1%; Score 1054; DB 2; Length 281;
 Best Local Similarity 96.8%; Pred. No. 7.9e-82;
 Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DSWMTSLNPLGTTVCLGNSQSPSTNSPTSCPTCPGYRMWCLARRPIIFILLCLII 60
 DB 88 DSWMTSLNPLGTTVCLGNSQSPSTNSPTSCPTCPGYRMWCLARRPIIFILLCLII 147
 QY 61 FLVLYLDYQGLPVCPLIPGSSSTTSKQCRCTTPAAGTSMYPSGCCCTKBDGCTCPIPI 120
 DB 148 FLVLYLDYQGLPVCPLIPGSSSTTSKQCRCTTPAAGTSMYPSGCCCTKBDGCTCPIPI 207
 QY 121 PSSWAFGKFLMEWASARFSLVLPVQWFGVLSPTVMVIMMMYMGSLYSLSLSPF 180
 DB 208 PSSWAFGKFLMEWASARFSLVLPVQWFGVLSPTVMVIMMMYMGSLYSLSLSPF 267
 QY 181 SPLLPFFC 189

Db 268 LPLPIFFC 276

RESULT 13

ID Q6XJ0 PRELIMINARY; PRT; 281 AA.

AC Q6XJ0; 06XJ0; 05-JUL-2004 (T-EMBLrel. 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Middle S protein.

OS Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA PubMed=15105537; DOI=10.1099/vir.0.19749-0;

RA Kimb G.C., Kramvis A., Kew M.C.;

RT "Distinctive sequence characteristics of subgenotype A1 isolates of hepatitis B virus from South Africa."

RL J. Gen. Virol. 85:1211-1220(2004).

DR EMBL; AY233293; AAP79851.1; -

DR GO; GO:0016032; P:Viral life cycle; IEA.

DR InterPro; IPR000349; Hepvir_surfAg.

DR Pfam; PF00695; VMSA; 1.

KW Antigen.

SQ SEQUENCE 281 AA; 31232 MW; 52325AB26590AEF8 CRC64;

Query Match 97.1%; Score 1054; DB 2; Length 281;

Best Local Similarity 96.8%; Pred. No. 7.9e-82;

Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSWMTSLNFIAGTTTVCIGQNSQSPTSNHSPTSCPTCPGRRMCLRRFIIFLLILCL 60

Db 88 DSWMTSLNFIAGTTTVCIGQNSQSPTSNHSPTSCPTCPGRRMCLRRFIIFLLILCL 147

Qy 61 FLVLLDYQGLPVCPLIPGSSSTTSKGCCTCTTPAQTSMYPSCCCTKPSDGNCTCIP 120

Db 148 FLVLLDYQGLPVCPLIPGSSSTTSKGCCTCTTPAQTSMYPSCCCTKPSDGNCTCIP 207

Qy 121 PSSMARGKYLMEWASARFWSLSLVPFVQMFVGLSPTWLSVIMMMYMGPSLYSILSP 180

Db 208 PSSMARGKYLMEWASARFWSLSLVPFVQMFVGLSPTWLSVIMMMYMGPSLYSILSP 267

Qy 181 SPLPIFFC 189

Db 268 LPLPIFFC 276

RESULT 14

ID Q9J1J6 PRELIMINARY; PRT; 281 AA.

AC Q9J1J6; 09J1J6; 01-OCT-2000 (T-EMBLrel. 15, Created)

DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Pres2-S protein.

OS Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20345625; PubMed=10884611; DOI=10.1016/S1286-4579(00)00365-8;

RA Borchani-Chabchoub I., Gargouri A., Mokdad-Gargouri R.;

RT "Genotyping of Tunisian hepatitis B virus isolates based on the RT sequencing of pres2 and S regions."

RL Microbes Infect. 2:607-612(2000).

DR EMBL; AF214661; AAP31270.1; -

DR PIR; JQ1572; JQ1572.

DR PIR; JQ2063; JQ2063.

DR PIR; JQ2066; JQ2066.

DR PIR; JQ2067; JQ2067.

DR PIR; JQ2068; JQ2068.

DR PIR; JQ2069; JQ2069.

DR PIR; JQ2070; JQ2070.

DR PIR; JQ2072; JQ2072.

DR PIR; JQ2076; JQ2076.

DR PIR; JQ2077; JQ2077.

DR PIR; JQ2079; JQ2079.

DR PIR; JQ2081; JQ2081.

DR PIR; JQ2083; JQ2083.

DR PIR; JQ2091; JQ2091.

DR PIR; JQ2092; JQ2092.

DR GO; GO:0016032; P:Viral life cycle; IEA.

DR InterPro; IPR000349; Hepvir_surfAg.

DR Pfam; PF00695; VMSA; 1.

KW Antigen.

FT CHAIN

SQ SEQUENCE 281 AA; 31270 MW; 673BC6C4902BP954 CRC64;

Query Match 97.1%; Score 1054; DB 2; Length 281;

Best Local Similarity 96.8%; Pred. No. 7.9e-82;

Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DSWMTSLNFIAGTTTVCIGQNSQSPTSNHSPTSCPTCPGRRMCLRRFIIFLLILCL 60

Db 88 DSWMTSLNFIAGTTTVCIGQNSQSPTSNHSPTSCPTCPGRRMCLRRFIIFLLILCL 147

Qy 61 FLVLLDYQGLPVCPLIPGSSSTTSKGCCTCTTPAQTSMYPSCCCTKPSDGNCTCIP 120

Db 148 FLVLLDYQGLPVCPLIPGSSSTTSKGCCTCTTPAQTSMYPSCCCTKPSDGNCTCIP 207

Qy 121 PSSMARGKYLMEWASARFWSLSLVPFVQMFVGLSPTWLSVIMMMYMGPSLYSILSP 180

Db 208 PSSMARGKYLMEWASARFWSLSLVPFVQMFVGLSPTWLSVIMMMYMGPSLYSILSP 267

Qy 181 SPLPIFFC 189

Db 268 LPLPIFFC 276

RESULT 15

ID Q9J1J7 PRELIMINARY; PRT; 281 AA.

AC Q9J1J7; 09J1J7; 01-OCT-2000 (T-EMBLrel. 15, Created)

DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)

DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)

DE Pres2-S protein.

OS Hepatitis B virus.

OC Viruses; Retroid viruses; Hepadnaviridae; Orthohepadnavirus.

OX NCBI_TaxID=10407;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=20345625; PubMed=10884611; DOI=10.1016/S1286-4579(00)00365-8;

RA Borchani-Chabchoub I., Gargouri A., Mokdad-Gargouri R.;

RT "Genotyping of Tunisian hepatitis B virus isolates based on the RT sequencing of pres2 and S regions."

RL Microbes Infect. 2:607-612(2000).

DR EMBL; AF214660; AAP31269.1; -

DR PIR; JQ1572; JQ1572.

DR PIR; JQ2063; JQ2063.

DR PIR; JQ2066; JQ2066.

DR PIR; JQ2067; JQ2067.

DR PIR; JQ2068; JQ2068.

DR PIR; JQ2069; JQ2069.

DR PIR; JQ2070; JQ2070.

DR PIR; JQ2072; JQ2072.

DR PIR; JQ2076; JQ2076.

DR PIR; JQ2077; JQ2077.

DR PIR; JQ2079; JQ2079.

DR PIR; JQ2081; JQ2081.

DR PIR; JQ2083; JQ2083.

DR PIR; JQ2091; JQ2091.

DR PIR; JQ2092; JQ2092.
 DR GO; GO:0016032; P:Viral life cycle; IEA.
 DR InterPro; IPR000349; Hepvir_surfac.
 DR Pfam; PF00695; VMSA; 1.
 DR Antigen.
 KW CHAIN
 FT CHAIN
 SQ SEQUENCE 261 AA; 31260 MW; F2325C86F7D9844E CRC64;

Query Match 97.1%; Score 1054; DB 2; Length 281;
 Best Local Similarity 96.8%; Pred. No. 7.9e-82;
 Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy	1	DSMTSLNPLAGSTTVCIGNSQSPNSH8PTSCPTCPGYRMWCLRRFIIIFILLCLI	60
Db	88	DSMTSLNPLAGSTTVCIGNSQSPNSH8PTSCPTCPGYRMWCLRRFIIIFILLCLI	147
Qy	61	FLVLVDYQGLPVCPLIPGSSSTSKGCRCTTPAQGTSMYPSCCCTKPSDNCICPI	120
Db	148	FLVLVDYQGLPVCPLIPGSSSTSKGCRCTTPAQGTSMYPSCCCTKPSDNCICPI	207
Qy	121	PSSWAFGKYLWEMASARFSLVLPVQMFVGLSPTVWLSVIWMMWYGPGLYSILSPF	180
Db	208	PSSWAFGKYLWEMASARFSLVLPVQMFVGLSPTVWLSVIWMMWYGPGLYSILSPF	267
Qy	181	SPILPIFC	189
Db	268	LPLPIFC	276

Search completed: July 25, 2005, 11:24:29
 Job time : 176 secs

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OM protein - protein search, using sw model

Run on: July 25, 2005, 11:01:26 ; Search time 164 Seconds
(without alignments)
445.718 Million cell updates/sec

Title: US-09-823-077C-7

Perfect score: 1085
Sequence: 1 DSWMTSLNFGTTCVLCIGN.....GPSLYSILSPFSLPLRIFPC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1054	97.1	229	6	ABP55076 Hepatitis
2	1054	97.1	347	3	ABP10596 HBV fusio
3	1046	96.4	226	4	AA62930 Amino aci
4	1046	96.4	309	7	ADG76903 Hepatitis
5	1046	96.4	389	4	AA66931 HBV genot
6	1046	96.4	389	4	AA66931 Amino aci
7	1045	96.3	226	2	AA66282 Hepatitis
8	1043	96.1	226	7	ADG06672 HBV envel
9	1041	95.9	226	7	ADG76900 Hepatitis
10	1040	95.9	226	5	AAE1897 Hepatitis
11	1040	95.9	226	7	ABM00348 Hepatitis
12	1040	95.9	249	3	AAV5245 Pan DR ep
13	1040	95.9	281	2	AAE19897 Hepatitis
14	1040	95.9	281	2	AAV32835 HBsAg Pre
15	1040	95.9	309	7	ADG76901 Hepatitis
16	1040	95.9	309	7	ADG76902 Hepatitis
17	1040	95.9	334	5	AAO22926 Hepatitis
18	1040	95.9	389	2	AAE27472 HBsAg SE7
19	1040	95.9	389	2	AAE27474 HBsAg pro
20	1040	95.9	389	6	ABO10262 HBV major
21	1040	95.9	393	4	AAU14097 Hepatitis
22	1040	95.9	397	2	AAW09048 Pleamid p
23	1037	95.6	226	1	AAPO0042 Sequence
24	1037	95.6	226	2	AAE06613 Hepatitis
25	1037	95.6	371	7	ADN02610 HBV N-ter

26	1037	95.6	389	7	ADN02608 HBV pres1
27	1033	95.2	203	1	AAPI0002 Sequence
28	1033	95.2	226	1	AAPI0001 Sequence
29	1033	95.2	226	2	AAW09045 Hepatitis
30	1033	95.2	229	6	ABP55075 Hepatitis
31	1033	95.2	276	2	AAW44780 Modified
32	1033	95.2	389	6	ABP55073 Hepatitis
33	1031	95.0	226	1	AAPO0005 Sequence
34	1031	95.0	226	1	AAE0374 Hepatitis
35	1030	94.9	226	5	ABP7764 Amino aci
36	1026	94.6	305	7	ADG06666 HBV envel
37	1014	93.5	325	7	ADG76917 Hepatitis
38	1010	93.1	309	7	ADG76918 Hepatitis
39	1009	93.0	197	7	ADG76914 Hepatitis
40	1007	92.8	226	2	AAE33252 HBsAg enc
41	1007	92.8	226	2	AAE5282 Deduced s
42	1007	92.8	251	2	AAE11495 HBsAg/HBs
43	1007	92.8	281	4	AAE02620 HBsAg pre
44	1007	92.8	389	2	AAE5287 Deduced s
45	1007	92.8	390	4	AAE02621 Chimeric

ALIGNMENTS

RESULT 1
ABP55076
ID ABP55076 standard; protein; 229 AA.
XX
AC ABP55076;
XX
DT 27-JAN-2003 (first entry)
XX
DE Hepatitis B virus wild-type small envelope protein.
XX
KW HBV; HBsAg; surface antigen; envelope; diagnosis; vaccine.
XX
OS Hepatitis b virus.
XX
PN WO200279217-A1.
XX
PD 10-OCT-2002.
XX
PF 26-MAR-2002; 2002WO-US009227.
XX
PR 30-MAR-2001; 2001US-00821877.
XX
PA (ABBO) ABBOTT LAB.
XX
PI Coleman PF, Mushahwar IA,
XX
DR WPI; 2003-040642/03.
XX
DR N-PSDB; ABV75785.
XX
PT New nucleotide sequences, useful for detecting compounds that bind to
PT gp41 protein or antibodies to the Hepatitis B virus surface antigen
PT mutant or for creating primers and probes.
XX
PS Claim 3; Fig 4A-B; 43pp; English.
XX
CC The present sequence is the protein sequence of the small envelope
CC protein of a wild-type hepatitis B virus (HBV) subtype ayw2 strain. The
CC invention relates to a mutated HBV ayw1 strain isolated from a French
CC sample and identified as 990525169. The mutant sequence (see ABP55075)
CC contains 3 mutations compared with the wild-type sequence: substitution
CC of alanine for the threonine residue at position 123; tryptophan for
CC leucine-199; and serine for threonine-207. The T123A substitution is
CC within the 'a' determinant region and affects the H166 epitope. The
CC present invention relates to the novel HBV mutant which has a modified
CC 'a' determinant as a result of T123A amino acid substitution, and to
CC methods of detecting this mutant, and/or antibodies to the mutant, in
CC patient samples. The identification and detection of mutant HBV may lead
CC to improved vaccine development and detection systems

3Q Sequence 229 AA;

Query Match 97.1%; Score 1054; DB 6; Length 229;
Best Local Similarity 96.8%; Pred. No. 1.2e-87;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

1 DSWMTSLNPLGTTVCIGONSQSPSTNSHPTSCPTCPGVRMCLRRFIIIFLFIILCLL 60
36 DSWMTSLNPLGTTVCIGONSQSPSTNSHPTSCPTCPGVRMCLRRFIIIFLFIILCLL 95
61 FLVLLDYOGILPVCPLIPSSSTTSKQCCRTCTTPAGTSMYPSCCCTKPSDGCCTCPI 120
96 FLVLLDYOGILPVCPLIPSSSTTSKQCCRTCTTPAGTSMYPSCCCTKPSDGCCTCPI 155
121 PSSWAFFGKILMWSARFSLVLPVQWVGSLPTVWLSVIMMMYWGPSLYSIIISPF 180
156 PSSWAFFGKILMWSARFSLVLPVQWVGSLPTVWLSVIMMMYWGPSLYSIIISPF 215
181 SPLPIFFPC 189
216 LPLPIFFPC 224

RESULT 2
AAB10596
ID AAB10596 standard; protein; 347 AA.

06-AUG-2003 (revised)
08-JAN-2001 (first entry)
HBV fusion protein comprising LHB and RGD.

Fusion protein; protein coat; virus-specific packaging signal; psi;
virus protein; cell permeability; cell-specific binding site; LHB;
large surface protein; core antigen; gene therapy.

Hepatitis B virus.
Synthetic.

MO200046376-A2.

10-AUG-2000.
04-FEB-2000; 2000MO-DE000363.
05-FEB-1999; 99DB-01004800.

(HILD/) HILDT E.
H1dE E, Hofschneider P;

WPI; 2000-514959/46.
N-PSDB; AAA71734.

Particle for cell-specific gene delivery, useful in gene therapy,
comprises nucleic acid in protein coat that includes a fusion protein of
viral protein, permeability peptide and cell-binding site.

Claim 14; Fig 1; 34pp; German.

This invention describes a novel particle (A), comprising a protein coat
with a fusion protein (FP), and, inside the coat, a nucleic acid (1) and a
including the sequence for a virus-specific packaging signal (psi) and a
structural gene. FP contains a virus protein (VP), a peptide (P) that
mediates cell permeability and a heterologous cell-specific binding site
(RGD). The invention also describes (1) producing (A) in which FP
contains an LHBs (large surface protein of hepatitis B virus (HBV)) and
containing an LHBs (large surface protein of hepatitis B virus (HBV)) and
(P) and RGD; (2) preparing (A) in which FP contains an HBV core antigen (HBCAg);
(P) and RGD; (3) FP; (4) DNA encoding FP; and (5) expression vector
containing the DNA of (d). The products of the invention are used in gene

CC therapy of cells and tissues, in vivo or ex vivo. This sequence
CC represents a fusion protein which is described in the method of the
CC invention. (updated on 06-AUG-2003 to correct OS field.)

3Q Sequence 347 AA;

Query Match 97.1%; Score 1054; DB 3; Length 347;
Best Local Similarity 96.8%; Pred. No. 1.9e-87;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

1 DSWMTSLNPLGTTVCIGONSQSPSTNSHPTSCPTCPGVRMCLRRFIIIFLFIILCLL 60
154 DSWMTSLNPLGTTVCIGONSQSPSTNSHPTSCPTCPGVRMCLRRFIIIFLFIILCLL 213
61 FLVLLDYOGILPVCPLIPSSSTTSKQCCRTCTTPAGTSMYPSCCCTKPSDGCCTCPI 120
214 FLVLLDYOGILPVCPLIPSSSTTSKQCCRTCTTPAGTSMYPSCCCTKPSDGCCTCPI 273
121 PSSWAFFGKILMWSARFSLVLPVQWVGSLPTVWLSVIMMMYWGPSLYSIIISPF 180
274 PSSWAFFGKILMWSARFSLVLPVQWVGSLPTVWLSVIMMMYWGPSLYSIIISPF 333
181 SPLPIFFPC 189
334 LPLPIFFPC 342

RESULT 3
AAG62930
ID AAG62930 standard; protein; 226 AA.

AAG62930;
17-SEP-2001 (first entry)

Amino acid sequence of a mutated HBV S gene antigen.

S gene; HBsAg; HBV; pre-S gene; C gene; P gene; X gene;
surface antigen; envelope protein; HBsAg; HBeAg; HBCAg; DNA polymerase;
reverse transcriptase; HBxAg; immune response; viral protein expression;
HBV infection.

Hepatitis B virus.

MO200149828-A1.

12-JUL-2001.

05-JAN-2001; 2001MO-FR000038.

06-JAN-2000; 2000FR-00000129.

(INRM) INSERM INST NAT SANTE & RECH MEDICALE.

(INMR) BIOMERIEUX SA.

Trepo C, Mandrand B, Kay A, Chemin I, Komurian-Pradel F;

WPI; 2001-441870/47.

New mutant of hepatitis B virus, useful for diagnosis, prevention and
treatment of infection, also related nucleic acids, proteins and
antibodies.

Claim 36; Page 92; 102pp; French.

The present sequence represents a mutated S gene antigen, designated
HBsm. It is part of the mutant hepatitis B virus (HBVB) of the invention,
which has a circular, partially double-stranded genome comprising pre-S,
S, C, P and X genes, encoding, respectively, surface antigens, envelope
protein (HBsAg), proteins HBeAg and HBCAg, DNA polymerase/reverse
transcriptase, and HBxAg. The mutant HBV of the invention are used for
induction of specific humoral or cellular immune responses, or antisense
inhibition of viral protein expression. Proteins and nucleic acids

CC derived from mHBV (also related antibodies, vectors, transformed cells
CC and oligonucleotides) are useful for diagnosis (in standard
CC amplification, hybridization or immune-complex forming assays) and for
CC treatment of, or vaccination against, HBV infection

XX Sequence 226 AA;

Query Match 96.4%; Score 1046; DB 4; Length 226;
Best Local Similarity 95.8%; Pred. No. 6.6e-87;
Matches 181; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSWMTSLNFIAGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCLL 60
DB 33 DSWMTSLNFIAGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCLL 92
QY 61 FLVLLDYGGILPVCPPLIPGSSSTTSKQCRCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 120
DB 93 FLVLLDYGGILPVCPPLIPGSSSTTSKQCRCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 152
QY 121 PSSNARGLTMEWASARFWSLSLVPVQWFGVLSPTWMLSVIWMWYMGPSLYSLSPF 180
DB 153 PSSNARGLTMEWASARFWSLSLVPVQWFGVLSPTWMLSVIWMWYMGPSLYSLSPF 212
QY 181 SPILLPIFFC 189
DB 213 LPILLPIFFC 221

RESULT 4
ADG76903
ID ADG76903 standard; protein, 309 AA.

XX ADG76903;

DT 11-MAR-2004 (first entry)

XX Hepatitis B virus envelope amino acid sequence Segid26.

XX hepatitis B virus; HBV; polymerase; ADV; LMV, TVF, PTC, ADV; LMV, ADV;
XX TVF; anti-HBV agent; hepatotropic; virucide; anti-inflammatory;
XX HBV variant polymerase-antagonist; gene therapy; viral component;
XX inhibiting infection; virus replication; virus release; envelope.

XX Hepatitis B virus.

XX Key Location/Qualifiers

XX Misc-difference 1. .309
XX /label= OTHER
XX /note= "OTHER= Any Xaa's in this sequence can be any
XX amino acid"

XX WO2003087351-A1.

XX 23-OCT-2003.

XX 11-APR-2003; 2003WO-AU000432.

XX 12-APR-2002; 2002AU-00001710.

XX 26-JUN-2002; 2002AU-00003224.

XX (MELB-) MELBOURNE HEALTH.

XX (AUST-) AUSTIN & REPARIATION MEDICAL CENT.

XX (SHEA-) SOUTHERN HEALTH.

XX Bartholomew AI, Locarnini SA, Ayres A, Colledge D, Sasadeusz J;

XX Tillmann H, Angus PW, Stevert W;

XX WPI; 2003-845324/78.

XX New isolated hepatitis B viral variants with reduced susceptibility to
XX nucleoside analogs, useful for screening and/or developing
XX agents capable of inhibiting infection, replication and/or release of the
XX virus.

XX Example 5; SEQ ID NO. 26; 268pp; English.

XX This invention relates to a novel isolated hepatitis B virus (HBV)
XX variant which comprises a nucleoside mutation in a gene encoding a DNA
XX polymerase resulting in at least one amino acid addition, substitution
XX and/or deletion to the polymerase, and exhibiting decreased sensitivity
XX to (for example) ADV, LMV, TVF, or PTC, or ADV and LMV, ADV and TVF,
XX and/or other nucleoside, analogues, anti-HBV agents or their
XX combinations. The invention may be useful for the development of
XX compounds with a hepatotropic, virucide or anti-inflammatory activity as
XX HBV variant polymerase-antagonists. In addition, the sequences may be
XX useful for gene therapy. The HBV variants or their component are useful
XX in the rational design of an anti-HBV agent comprising microarray
XX analysis and is based on the crystal structure or NMR structure of a
XX viral component. The methods and compositions of the present invention
XX are also useful for screening, designing and/or developing agents capable
XX of inhibiting infection, replication and/or release of the virus.

XX Sequence 309 AA;

Query Match 96.4%; Score 1046; DB 7; Length 309;
Best Local Similarity 96.3%; Pred. No. 9.1e-87;
Matches 182; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSWMTSLNFIAGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCLL 60
DB 116 DSWMTSLNFIAGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCLL 175
QY 61 FLVLLDYGGILPVCPPLIPGSSSTTSKQCRCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 120
DB 176 FLVLLDYGGILPVCPPLIPGSSSTTSKQCRCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 235
QY 121 PSSNARGLTMEWASARFWSLSLVPVQWFGVLSPTWMLSVIWMWYMGPSLYSLSPF 180
DB 236 PSSNARGLTMEWASARFWSLSLVPVQWFGVLSPTWMLSVIWMWYMGPSLYSLSPF 295
QY 181 SPILLPIFFC 189
DB 296 LPILLPIFFC 304

RESULT 5

XX AAG66931
ID AAG66931 standard; protein, 389 AA.

XX AAG66931;

XX 19-OCT-2001 (first entry)

XX HBV genotype D pres1/pres2/HBsAg polypeptide.

XX Hepatitis B virus; HBV; preCore; Core; pres1; pres2; HBs; HBx; HBp1;
XX HBsAg; antiviral; vaccine; genotype G; genotyping; HBcAg; HBsAg.

XX Hepatitis B virus.

XX WO200140279-A2.

XX 07-JUN-2001.

XX 20-NOV-2000; 2000WO-EP011526.

XX 03-DEC-1999; 99EP-00870252.

XX 07-DEC-1999; 99US-0169287P.

XX (INNO-) INNOGENETICS NV.

XX Stuyver L, Van Geyt C, De Gendt S;

XX WPI; 2001-374785/39.

XX Novel isolated and/or purified hepatitis B virus polypeptide and

PT polynucleotide sequences that are phylogenetically different from HBV
PT genotype A-F molecules, useful for HBV diagnostics, prophylaxis and
therapy.

Example 3, Fig 6, 94pp; English.

The invention relates to the complete nucleic acid sequence of a new
human hepatitis B virus (HBV) genotype, provisionally named genotype G.
This genotype was found with a high prevalence in patients chronically
infected with HBV and residing in Europe and the USA. The invention
relates to a fully defined sequence of 3248 nucleotides as given in
specification, a sequence with 92% identity to the given sequence, or
sequence that is degenerate to the mentioned sequences. These
polynucleotides are useful for HBV genotyping. The proteins encoded by
the polynucleotides are useful for detecting antibodies in a biological
sample. Ligands that bind to the proteins and antibodies directed against
the proteins are useful for detecting the proteins and for detecting
HBsAg and HBeAg (precursor proteins). They are also useful for
preparing a vaccine or medicament for treating HBV infections. The
present sequence is provided in an amino acid sequence alignment of the
preS1, preS2 and HBeAg open reading frame of the different HBV genotypes

Sequence 389 AA;

Query Match 96.4%; Score 1046; DB 4; Length 389;
Best Local Similarity 96.3%; Pred. No. 1.2e-86;
Matches 182; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSWMTSLNFIAGTTCVCLGQNSQSPSTNSHSPSCPTCGYRMCLRRRIIFLFIILLCLI 60
DB 196 DSWMTSLNFIAGTTCVCLGQNSQSPSTNSHSPSCPTCGYRMCLRRRIIFLFIILLCLI 255
QY 61 FLVLVDYQGLIPVCPILPGSSTTSKGCRCCTTPAOGTSMYPSCCTKPSDGNCTCIP 120
DB 256 FLVLVDYQGLIPVCPILPGSSTTSKGCRCCTTPAOGTSMYPSCCTKPSDGNCTCIP 315
QY 121 PSSNAFGKYLWEMASARPSWLSLVFQVFGVGLSPYVWLSVIMWMTWGP8LYSILSPF 180
DB 316 PSSNAFGKYLWEMASARPSWLSLVFQVFGVGLSPYVWLSVIMWMTWGP8LYSILSPF 375
QY 181 SPLLPFPFC 189
DB 376 LPLLPFPFC 384

RESULT 6
AA62931

ID AAG62931 standard; protein; 389 AA.

AC AAG62931;

DT 17-SEP-2001 (first entry)

DE Amino acid sequence of a mutated HBV Pre-S protein.

XX S gene; HBem; mHBV; HBV; pre-S gene; C gene; P gene; X gene;
XX surface antigen; envelope protein; HBeAg; HBeAg; HBeAg; DNA polymerase;
XX reverse transcriptase; HBsAg; immune response; viral protein expression;
KW HBV infection.

OS Hepatitis B virus.

PN WO200149828-A1.

PD 12-JUL-2001.

PF 05-JAN-2001; 2001WO-FR000038.

PR 06-JAN-2000; 2000FR-00000129.

PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (INRM) BIOMERIEUX SA.

PI Trepo C, Mandrand B, Kay A, Chemin I, Komurian-Pradel F,
XX WPI; 2001-441870/47.

PT New mutant of hepatitis B virus, useful for diagnosis, prevention and
PT treatment of infection, also related nucleic acids, proteins and
PT antibodies.

PS Claim 36; Page 92-94; 102pp; French.

The present sequence represents a mutated Pre-S gene. It is part of the
mutant hepatitis B virus (mHBV) of the invention, which has a circular,
partially double-stranded genome comprising pre-S, S, C, P and X genes,
encoding, respectively, surface antigens, envelope protein (HBsAg),
proteins HBeAg and HBeAg, DNA polymerase/reverse transcriptase, and
HBsAg. The mutant HBV of the invention are used for induction of specific
humoral or cellular immune responses, or antisense inhibition of viral
protein expression. Proteins and nucleic acids derived from mHBV (also
related antibodies, vectors, transformed cells and oligonucleotides) are
useful for diagnosis (in standard amplification, hybridization or immune-
complex forming assays) and for treatment of, or vaccination against, HBV
infection.

Sequence 389 AA;

Query Match 96.4%; Score 1046; DB 4; Length 389;
Best Local Similarity 95.8%; Pred. No. 1.2e-86;
Matches 181; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSWMTSLNFIAGTTCVCLGQNSQSPSTNSHSPSCPTCGYRMCLRRRIIFLFIILLCLI 60
DB 196 DSWMTSLNFIAGTTCVCLGQNSQSPSTNSHSPSCPTCGYRMCLRRRIIFLFIILLCLI 255
QY 61 FLVLVDYQGLIPVCPILPGSSTTSKGCRCCTTPAOGTSMYPSCCTKPSDGNCTCIP 120
DB 256 FLVLVDYQGLIPVCPILPGSSTTSKGCRCCTTPAOGTSMYPSCCTKPSDGNCTCIP 315
QY 121 PSSNAFGKYLWEMASARPSWLSLVFQVFGVGLSPYVWLSVIMWMTWGP8LYSILSPF 180
DB 316 PSSNAFGKYLWEMASARPSWLSLVFQVFGVGLSPYVWLSVIMWMTWGP8LYSILSPF 375
QY 181 SPLLPFPFC 189
DB 376 LPLLPFPFC 384

RESULT 7
AA62826

ID AAW62826 standard; protein; 226 AA.

AC AAW62826;

DT 26-OCT-1998 (first entry)

DE Hepatitis B virus surface antigen.

XX Hepatitis delta virus; L-HAg; virus-like particle; infection;
XX hepatitis delta antigen; HBeAg; immune response; vaccine.

OS Hepatitis B virus.

PN WO9828004-A1.

PD 02-JUL-1998.

PF 24-DEC-1997; 97WO-AU000884.

PR 24-DEC-1996; 96AU-00004341.

PA (QUEB-) QUEBENS LAND DEPT HEALTH SAKZEMSKI VIRUS.

PA Gowans EJ, Macnaughton TB;

DR .WPI; 1998-377411/32.
DR N-PSDB; AAV42306.

PT Virus-like particle for, e.g. treating microbial infection - comprises polypeptide from microorganism and sequence from Hepatitis D virus large protein, partially enveloped by Hepatitis B surface antigen.

PS Example; Fig 6; 72pp; English.

CC This polypeptide comprises a hepatitis B virus surface antigen (HBsAg) encoded by the DNA insert (see AAV42306) of plasmid pTM-HBsAg. The invention provides a virus-like particle (VLP) comprising an antigenic and/or immunogenic polypeptide from a microorganism (e.g. hepatitis C virus) fused to at least the last 19 amino acids (see AAV62827) of the C-terminal sequence of the large protein from hepatitis D virus (L-HDag), in which the fusion protein is packaged into VLPs through the interaction of the L-HDag moiety with HBsAg. The VLP is used to ameliorate or protect against infections caused by hepatitis B virus and/or another microorganism.

CC Sequence 226 AA;

Query Match 96.3%; Score 1045; DB 2; Length 226;
Best Local Similarity 95.8%; Pred. No. 8.1e-87;
Matches 181; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSWMTSLNLTGTTVCLGNSQSPSTNSHPTSCPPCPGKRMCLRRFIFLILLCL 60
DB 33 DSWMTSLNLTGTTVCLGNSQSPSTNSHPTSCPPCPGKRMCLRRFIFLILLCL 92
QY 61 FLVLLDYGGILPVCPGLIGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDNCICPI 120
DB 93 FLVLLDYGGILPVCPGLIGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDNCICPI 152
QY 121 PSSMAFGKYLMEVNASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLSYLSLSPF 180
DB 153 PSSMAFGKYLMEVNASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLSYLSLSPF 212
QY 181 SPLLPFFC 189
DB 213 LPLLPFFC 221

RESULT 8

ADC06672
ID ADC06672 standard; protein; 226 AA.

AC ADC06672;

DT 18-DEC-2003 (first entry)

DE HBV envelope gene protein from patient B on-ETV therapy.

KM HBV; entecavir; ETV; lamivudine((-)-beta-2'-deoxy-3'-thiacytidine);

KW lamivudine; LMV; 3TC; virucide; antiinflammatory; hepatotropic;

KM nucleoside analogue resistance; vaccine; HBsAg; envelope;

OS Hepatitis B virus.

PN MO2003066841-A1.

PD 14-AUG-2003.

PF 05-FEB-2003; 2003MO-AU000111.

PR 07-FEB-2002; 2002AU-00000370.

PA 21-MAR-2002; 2002AU-00001269.

XX (MELB-) MELBOURNE HEALTH.
XX (AUST-) AUSTIN & REPARATION MEDICAL CENT.
XX (SHEA-) SOUTHERN HEALTH.

PI Bartholomewuz AI, Locarnini SA, Ayres A, Angus PW, Sievert W;
XX WPI; 2003-663592/62.

PT New variants of hepatitis B virus resistant to nucleoside analogs, useful in vaccines and for screening to detect therapeutic inhibitors.

PS Example 5; Fig 10; 124pp; English.

CC The invention relates to a novel isolated hepatitis B virus (HBV) variant comprising a nucleoside mutation in a DNA polymerase gene resulting in at least one amino acid addition, substitution and/or deletion, where the variant has reduced sensitivity to entecavir (ETV) or lamivudine((-)-beta-2'-deoxy-3'-thiacytidine) (LMV or 3TC). The variant of the invention demonstrates virucide, antiinflammatory and hepatotropic activities and may be useful for treating and monitoring nucleoside analogue-resistant HBV infections, in screening for therapeutic agents or in the rational design of such agents, as well as in the design of vaccines. The current sequence is that of the HBV envelope gene protein (HBsAg; Hepatitis B surface antigen) of the invention which was isolated from patient B during ETV therapy.

CC Sequence 226 AA;

Query Match 96.1%; Score 1043; DB 7; Length 226;
Best Local Similarity 95.2%; Pred. No. 1.2e-86;
Matches 180; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 DSWMTSLNLTGTTVCLGNSQSPSTNSHPTSCPPCPGKRMCLRRFIFLILLCL 60
DB 33 DSWMTSLNLTGTTVCLGNSQSPSTNSHPTSCPPCPGKRMCLRRFIFLILLCL 92
QY 61 FLVLLDYGGILPVCPGLIGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDNCICPI 120
DB 93 FLVLLDYGGILPVCPGLIGSSSTTSKQCRCTTPAOGTSMYPSCCCTKPSDNCICPI 152
QY 121 PSSMAFGKYLMEVNASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLSYLSLSPF 180
DB 153 PSSMAFGKYLMEVNASARFSLVLPVQMFVGLSPTVWLSVIMMMYMGPSLSYLSLSPF 212
QY 181 SPLLPFFC 189
DB 213 LPLLPFFC 221

RESULT 9

ADG76900
ID ADG76900 standard; protein; 226 AA.

AC ADG76900;

DT 11-MAR-2004 (first entry)

DE Hepatitis B virus envelope amino acid sequence SeqID23.

KM hepatitis B virus; HBV; polymerase; ADV; LMV; TV; ETV; ADV; LMV; ADV;

KW TV; anti-HBV agent; hepatotropic; virucide; antiinflammatory;

KM HBV variant polymerase-antagonist; gene therapy; viral component;

OS inhibiting infection; virus replication; virus release; envelope.

PN Hepatitis B virus.

FT Key Location/Qualifiers
FT Misc-difference 1. .226
FT /label= OTHER
FT /note= "OTHER= Any Xaa's in this sequence can be any amino acid"

PN MO2003087351-A1.

PD 23-OCT-2003.

PF 11-APR-2003; 2003MO-AU000432.

XX 12-APR-2002; 2002AU-00001710.
PR 26-JUN-2002; 2002AU-00003224.
XX
XX
PA (MELB-) MELBOURNE HEALTH.
PA (AUST-) AUSTIN & REPARATION MEDICAL CENT.
PA (SHEA-) SOUTHERN HEALTH.
XX
PI Bartholomewus AI, Locarnini SA, Ayres A, Colledge D, Sasadeusz J,
PI Tilmann H, Angus PW, Stevert W,
XX
DR WPI; 2003-845324/78.
XX
PT New isolated hepatitis B viral variants with reduced susceptibility to
PT nucleoside analogs, useful for screening, designing and/or developing
PT agents capable of inhibiting infection, replication and/or release of the
PT virus.
XX
XX
XX Example 5; SEQ ID NO 23; 268bp; English.
XX
XX This invention relates to a novel isolated hepatitis B virus (HBV)
XX variant which comprises a nucleoside mutation in a gene encoding a DNA
XX polymerase resulting in at least one amino acid addition, substitution
XX and/or deletion to the polymerase, and exhibiting decreased sensitivity
XX to (for example) ADV, LMV, TFPV, or PFC, or ADV and LMV, ADV and TFPV,
XX and/or other nucleoside analogues, anti-HBV agents or their
XX combinations. The invention may be useful for the development of
XX compounds with a hepatotropic, virucide or antiinflammatory activity as
XX HBV variant polymerase-antagonists. In addition, the sequences may be
XX useful for gene therapy. The HBV variants or their component are useful
XX in the rational design of an anti-HBV agent comprising microarray
XX analysis and is based on the crystal structure or NMR structure of a
XX viral component. The methods and compositions of the present invention
XX of inhibiting infection, replication and/or release of the virus.
XX
SQ Sequence 226 AA;
XX
Query Match 95.9%; Score 1041; DB 7; Length 226;
Best Local Similarity 95.8%; Pred. No. 1.9e-86;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 DSWMTSLNFIAGTTCVCGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLFIILCL 60
Db 33 DSWMTSLNFIAGTTCVCGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLFIILCL 92
QY 61 FLVLADYQGIPLVCPILPSSSTTSKQCRCTTTPAQTSMYPSGCCCKRSDGCTCIP 120
Db 93 FLVLADYQGMPLVCPILPSSSTTSKQCRCTTTPAQTSMYPSGCCCKRSDGCTCIP 152
QY 121 PSSWAQKTYLMEWASARFWSLVLVFPVQVFGISPTVWLSVIMMMYWGPSLYSILSPF 180
Db 153 PSSWAQKTYLMEWASARFWSLVLVFPVQVFGISPTVWLSVIMMMYWGPSLYSILSPF 212
QY 181 SPILPIFFC 189
Db 213 LPILPIFFC 221
XX
RESULT 10
AAE19897
ID AAE19897 standard; protein; 226 AA.
XX
XX AAE19897;
XX
XX 18-JUN-2002 (first entry)
XX
XX Hepatitis B virus S antigen (HBsAg) sequence.
XX
XX Hepatitis B virus; HBV, infection; virucide; fungicide; antibacterial;
XX cytostatic; immunostimulant; vaccine; ribavirin; immune response; cancer.
XX
XX Hepatitis B virus.
XX
XX

XX WO200213855-A2.
PN
XX 21-FEB-2002.
PD
XX
XX 15-AUG-2001; 2001WO-IB001808.
PR
XX 17-AUG-2000; 2000US-0225767P.
PR 29-AUG-2000; 2000US-0229175P.
PR 03-NOV-2000; 2000US-00705547.
XX
XX (TRIP-) TRIP AB.
XX
XX Salberg M, Hultgren C;
XX
XX WPI; 2002-241837/29.
XX
XX
XX Vaccine compositions for treating and preventing disease, preferably
XX hepatitis C virus infection, comprises ribavirin and antigen that has
XX epitope present in hepatitis C virus.
XX
XX
XX Claim 11; Page 81; 120bp; English.
XX
XX The invention relates to a composition comprising ribavirin and an
XX antigen preferably non structural 3 protein (NS3)/4A fragment of HCV
XX hepatitis C virus (HCV) genome or a peptide or nucleic acid of HCV
XX sequence. The composition is useful for enhancing an immune response to a
XX hepatitis C antigen in humans, domestic, sport or pet species and as
XX vaccines for treating and preventing HCV infections. The composition is
XX also useful for treating viral, bacterial, fungal diseases and cancer.
XX The present sequence is Hepatitis B virus S antigen (HBsAg) sequence
XX
SQ Sequence 226 AA;
XX
Query Match 95.9%; Score 1040; DB 5; Length 226;
Best Local Similarity 95.8%; Pred. No. 2.3e-86;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 DSWMTSLNFIAGTTCVCGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLFIILCL 60
Db 33 DSWMTSLNFIAGTTCVCGNSQSPSTNSHSPSCPTCPGYRMCLRRFIIFLFIILCL 92
QY 61 FLVLADYQGIPLVCPILPSSSTTSKQCRCTTTPAQTSMYPSGCCCKRSDGCTCIP 120
Db 93 FLVLADYQGMPLVCPILPSSSTTSKQCRCTTTPAQTSMYPSGCCCKRSDGCTCIP 152
QY 121 PSSWAQKTYLMEWASARFWSLVLVFPVQVFGISPTVWLSVIMMMYWGPSLYSILSPF 180
Db 153 PSSWAQKTYLMEWASARFWSLVLVFPVQVFGISPTVWLSVIMMMYWGPSLYSILSPF 212
QY 181 SPILPIFFC 189
Db 213 LPILPIFFC 221
XX
RESULT 11
ABW00348
ID ABW00348 standard; protein; 226 AA.
XX
XX ABW00348;
XX
XX 15-JAN-2004 (first entry)
XX
XX Hepatitis B virus S antigen (HBsAg).
XX
XX Ribavirin; vaccine; immune response; infection; therapy; immunostimulant;
XX virucide.
XX
XX Hepatitis B virus.
XX
XX US2002136740-A1.
PN
XX
XX 26-SEP-2002.
XX

XX	15-AUG-2001; 2001US-00929955.
PF	
XX	
PR	17-AUG-2000; 2000US-0225767P.
XX	
PR	29-AUG-2000; 2000US-0229175P.
XX	
PA	(SALT/) SALLBERG M.
PA	(HULT/) HULTGREN C.
PI	Sallberg M, Hultgren C;
XX	
DR	WPI; 2003-764978/72.
XX	
PT	Vaccine compositions for treating and preventing disease, preferably
FT	hepatitis C virus infection, comprises ribavirin and antigen that has
PT	epitope present in hepatitis C virus.
XX	
PS	Claim 11; Page 44; 0pp; English.
XX	
CC	The invention relates to a composition comprising ribavirin and an
CC	antigen, where the antigen is derived from a hepatitis virus. The vaccine
CC	is useful in enhancing the immune response to a hepatitis C antigen where
CC	the composition is delivered to an animal identified as requiring an
CC	enhanced immune response. The vaccine is useful in the treatment and
CC	prevention of hepatitis C infection. The present sequence is Hepatitis B
CC	virus S antigen (HBsAg)
XX	
SO	Sequence 226 AA;
NY	Query Match 95.9%; Score 1040; DB 7; Length 226;
Dy	Best local similarity 95.8%; Pred. No. 2.3e-86;
Match	Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0
OY	1 DSWMTSLNPLGGTTVCLGNSQSPSTNSHPSCPTCPGYRMCRLRPFIPLFILLGLI 60
Db	33 DSWMTSLNPLGGTTVCLGNSQSPSTNSHPSCPTCPGYRMCRLRPFIPLFILLGLI 92
OY	61 FLVLVDYOGIIIPVCPILPGSSSTTSKQCRTCTTPAQTSMYPSCCCTYPDGNCTCIP I 120
Db	93 FLVLVDYOGIIIPVCPILPGSSSTTSKQCRTCTTPAQTSMYPSCCCTYPDGNCTCIP I 152
OY	121 PSSNAFGKYLWMASARFSKLSLVFYQVFYGAPTWLASYIMMMWVGPSLYISLPF 180
Db	153 PSSNAFGKFLWMAARFESWLIVFYQVFVGLSPTVMSIIMMMWVGPSLYISLPF 212
OY	181 SPLPLPFC 189
Db	213 LPLPLPFC 221
RESULT 12	
ID	AAVS2545 standard; protein; 249 AA.
AC	AAVS2545;
DT	06-AUG-2003 (revised)
DT	28-FEB-2000 (first entry)
DE	Pan DR epitope/HBV surface antigen fusion protein.
XX	
XX	Chimeric; HBV, surface antigen; pan DR epitope; expression vector;
KM	promoter; major histocompatibility complex; MHC; targeting; peptide;
KM	epitope; antigen; presentation; class I; cytosolic pathway;
KM	endoplasmic reticulum; class II; extracellular antigen;
KM	endocytic pathway; helper T lymphocyte; HTL; universal epitope;
KM	cytotoxic T lymphocyte; CTL; immune response; immunogenicity; assay;
KM	vaccine; immunity; infection; pathogen; virus; HIV; HBV; HCV;
KM	hepatitis B; hepatitis C; bacterium; protozoan; tumour cell;
KM	autoimmune disease; activation; antiviral; antimalarial;
KM	immunoprotective.
XX	
XX	Synthetic.

XX	Hepatitis B virus.
XX	
XX	NO9358658-A2.
XX	
PD	18-NOV-1999.
XX	
PF	13-MAY-1999; 99WO-US010646.
XX	
FR	13-MAY-1998; 98US-00078904.
XX	
PA	15-MAY-1998; 98US-0085751P.
XX	
PA	(EPIM-) EPIMMUNE INC.
XX	
P1	Fikes JD, Hermanson GG, Sette A, Ishloka GY, Livingston B;
XX	Chestnut KM;
DR	WPI; 2000-039103/03.
XX	N-PSDB; AAZ38623.
XX	
PT	Expression vectors encoding major histocompatibility targeting sequence,
XX	used as, e.g. tumor vaccines.
PS	
XX	Example 1; Fig 8; 130pp; English.
CC	This sequence represents the fusion protein encoded by a pan DR
CC	epitope/HBV surface antigen fusion gene, pADR-HBV-s, used in an
CC	exemplification of the present invention. The invention relates to a
CC	novel expression vector comprising a promoter operably linked to a fusion
CC	gene encoding a major histocompatibility complex (MHC) targeting
CC	sequence, and two or more heterologous peptide epitopes. The MHC
CC	targeting sequence may be a class I targeting sequence, which directs
CC	an MHC class I epitope to a cytosolic pathway or to the endoplasmic
CC	reticulum, or an MHC class II targeting sequence, which directs
CC	extracellular antigens to enter the endocytic pathway to be processed
CC	into antigen peptides for presentation on MHC class II molecules. The
CC	heterologous epitopes may comprise either helper T lymphocyte (HTL),
CC	epitopes, or a cytotoxic T lymphocyte (CTL) epitope and a universal HTL
CC	epitope such as a pan DR epitope (PADR). The vectors are useful for
CC	stimulating an immune response in vivo, as well as for use in assaying
CC	the human immunogenicity of a human T cell peptide epitope in vivo in a
CC	non-human mammal. They provide a nucleic acid vaccine for enhancing
CC	immunity against infectious pathogens, such as viruses (e.g., HIV,
CC	hepatitis B (HBV) and hepatitis C (HCV)) bacteria, protozoa (e.g.,
CC	Plasmodium falciparum, the cause of malaria) and also tumour cells and
CC	autoimmune diseases. Universal MHC class II epitopes are advantageously
CC	combined with other MHC class I and class II epitopes to increase the
CC	number of cells that are activated in response to a given antigen and
CC	provide a broader population coverage of MHC-reactive alleles. (Updated
CC	on 06-AUG-2003 to correct OS field.)
SC	
XX	
SC	Sequence 249 AA;
Query Match	95.9%; Score 1040; DB 3; Length 249;
Best Local Similarity	95.8%; Pred. No. 2.5e-86;
Matches 181; Conservative	2; Mismatches 6; Indels 0; Gaps 0;
DQ	1 DSWWTSLNPLGDTTVICLGONSQSPSTNSPTSCPEPTCGRYMMCLRRPILFLFIILLCLI 60
DB	56 DSWMTSLNPLGDTTVICLGONSQSPSTNSPTSCPEPTCGRYMMCLRRPILFLFIILLCLI 115
DQ	61 FLVLVDLYOGLIPVCPPLPGSSTTSKQCRCCTTPAQGTSMYPBSCCKRKBDAGNTCPI 120
DB	116 FLVLVDLYOGLIPVCPPLPGSSTTSKQCRCCTTPAQGTSMYPBSCCKRKBDAGNTCPI 175
DQ	121 PSSNAFGXCLMENASARPSMSLVFQGVIGASPVTWLAVIWMATNGESLSYSILSPF 180
DB	176 PSSNAFGXCLMENASARPSMSLVFQGVIGASPTVMASVINMMATNGESLSYSILSPF 235
DQ	181 SPLPLIFPC 189
DB	236 LPLPLIFPC 244

RESULT 13
 AAR27471
 ID AAR27471 standard; protein, 281 AA.
 XX
 AC AAR27471;
 XX
 DT 25-MAR-2003 (revised)
 DT 24-FEB-1993 (first entry)
 XX
 DE spsAg protein.
 XX
 KW Hepatitis B virus; HBV; M protein; small pre-S antigen; spsAg;
 KW vaccinia virus; H6; early/late; promoter; NVAC; recombinant; HBV L;
 KW large pre-S antigen; lpsAg; fusion protein; pre-S region; S12/core; S1;
 KW S2; Copenhagen vaccine strain; vaccinia virus; virulence factor;
 KW deletion loci; recipient loci.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Region 1..55
 FT /label= S2
 FT 56..281
 FT Region /label= S
 XX
 FN W09215672-A1.
 XX
 PD 17-SEP-1992.
 XX
 PF 09-MAR-1992; 92WO-US001906.
 XX
 PR 07-MAR-1991; 91US-00666056.
 PR 11-JUN-1991; 91US-00713967.
 PR 06-MAR-1992; 92US-00847951.
 XX
 PA (VIBRO-) VIBROGENETICS CORP.
 XX
 PI Paolucci B, Perkins ME, Taylor J, Tartaglia J, Norton EK,
 PI Riviere M, De Taisne C, Limbach KJ, Johnson GP, Pincus SE, Cox WJ,
 PI Francis J, Gettig RR;
 DR WPI: 1992-331718/40.
 DR N-PSDB; MAQ29103.
 XX
 FT Vaccine comprises recombinant, attenuated pox-virus - use for vaccinating
 PT against viral infections such as rabies, hepatitis B, HIV, HSV, EBV, CMV,
 PT mumps etc.
 XX
 PS Disclosure; Fig 9; 456pp; English.
 XX
 CC The sequence given is encoded by an expression cassette which consists of
 CC the hepatitis B virus (HBV) M protein (small pre-S antigen, spsAg) gene
 CC precisely linked to a modified synthetic vaccinia virus H6 early/late
 CC promoter. This DNA sequence was used in the construction of a NVAC
 CC recombinant expressing the HBV gene. Other HBV genes were also used in
 CC the construction. These were HBV L (large pre-S antigen, lpsAg) and a
 CC fusion protein composed of the entire pre-S region (S12/core, S1 + S2).
 CC Each of these gene sequences were inserted individually into three
 CC different sites of NVAC separated by from each other by large regions of
 CC vaccinia DNA containing essential genes. NVAC is a Copenhagen vaccine
 CC strain of vaccinia virus which has been modified by deletion of six non-
 CC essential regions of the genome encoding known or potential virulence
 CC factors. The deletion loci were engineered as recipient loci for the
 CC insertion of foreign genes. The spacing of the three inserted sequences
 CC ensured that any recombination that did occur would lead to disruption of
 CC the vaccinia genome and would cause unviable vaccinia virus. See also
 CC MAQ35501-864. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 281 AA;
 Query March 95.9%; Score 1040; DB 2; Length 281;
 Best Local Similarity 95.8%; Pred. No. 2.9e-86;
 Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLAGSTTVCLGQNSQPTSNHSPSCPTCGCYWMCARRIFILFILLCLL 60
 DB 88 DSWMTSLNPLAGSTTVCLGQNSQPTSNHSPSCPTCGCYWMCARRIFILFILLCLL 147
 QY 61 FLVLLDYQGLIPVCPILIPGSSITSSKQCCTCTTPAQGTSMYPSGCCPTSDGNTCIP 120
 DB 148 FLVLLDYQGLIPVCPILIPGSSITSSKQCCTCTTPAQGTSMYPSGCCPTSDGNTCIP 207
 QY 121 PSSWAFGKYLWEMASARPSWLSLVPPVQWFGSLPTVWLSVIMMWYWGSLYSILSP 180
 DB 208 PSSWAFGKYLWEMASARPSWLSLVPPVQWFGSLPTVWLSVIMMWYWGSLYSILSP 267
 QY 181 SPLPLPFC 189
 DB 268 LPLPLPFC 276
 RESULT 14
 AAY32835
 ID AAY32835 standard; protein, 281 AA.
 XX
 AC AAY32835;
 XX
 DT 27-AUG-2003 (revised)
 DT 29-OCT-1999 (first entry)
 XX
 DE HBsAg PreS2-S region protein sequence.
 XX
 KW HBsAg; PreS2-S; recombinant antigen library; disease-related antigen;
 KW multivalent antigenic polypeptide production; infection; allergen;
 KW asthma; autoimmune disease; rheumatoid arthritis; diabetes; therapy;
 KW multiple sclerosis; inflammatory condition; cancer; contraception;
 KW immune response; hepatitis b surface antigen.
 XX
 OS Hepatitis B virus.
 XX
 FN W09941383-A1.
 XX
 PD 19-AUG-1999.
 XX
 PF 10-FEB-1999; 99WO-US002944.
 XX
 PR 11-FEB-1998; 98US-00021769.
 PR 11-FEB-1998; 98US-0074234P.
 PR 23-OCT-1998; 98US-0105509P.
 XX
 PA (MAXY-) MAXYGEN INC.
 XX
 PI Punnonen J, Baas SH, Whalen RG, Howard R, Stemmer WPC;
 DR WPI: 1999-518452/43.
 DR N-PSDB; MAZ10968.
 XX
 FT Recombinant multivalent antigenic polypeptide produced by recombining
 PT nucleic acid sequences and screening; used in vaccines against e.g.
 PT infections and cancer.
 XX
 PS Example 14; Fig 17; 153pp; English.
 XX
 CC This sequence is the hepatitis B virus (HBV) surface antigen (HBsAg)
 CC PreS2-S region. This sequence was used to create a recombinant antigen
 CC library. The library comprises recombinant nucleic acids encoding
 CC antigenic polypeptides and is produced by recombination of at least two
 CC forms of nucleic acid, differing by at least two nucleotides, encoding a
 CC disease-related antigenic polypeptide. The library can be used to produce
 CC a recombinant multivalent antigenic polypeptides of the invention, that
 CC contains at least two antigenic determinants (AD) from different
 CC polypeptides. The multivalent antigenic polypeptides are used in vaccines
 CC to induce a protective or therapeutic response to a wide variety of
 CC infectious agents (bacteria, viruses, parasites, including Plasmodium
 CC falciparum); allergens; asthma; autoimmune disease (e.g. rheumatoid
 CC arthritis, diabetes, multiple sclerosis); other inflammatory conditions

CC and cancer, also, where directed against sperm antigens, they can be used
CC for contraception. The multivalent peptides can be evolved to induce an
CC optimized immune response against a wide variety of antigens,
CC particularly a broad spectrum response to many different strains of a
CC pathogen, including strains that are likely to appear in the future.
CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 281 AA;

Query Match 95.9%; Score 1040; DB 2; Length 281;

Best Local Similarity 95.8%; Pred. No. 2.9e-86; Indels 0; Gaps 0;

Matches 181; Conservative 2; Mismatches 6;

QY 1 DSMWTSINFLGGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCL 60
DB DSMWTSINFLGGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCL 147

QY 61 FLVVLDDYQGLPVCPLIPGSSITTSKQCRCTCTPAQGTSMYPSCCCTPSPDNCICPI 120
DB FLVVLDDYQGLPVCPLIPGSSITTSKQCRCTCTPAQGTSMYPSCCCTPSPDNCICPI 207

QY 121 PSSMAFGKYLMEWASARFSWLSLVFPVQWFGLSPTVWLSYIMMMYWGPSLYSLSPF 180
DB PSSMAFGKYLMEWASARFSWLSLVFPVQWFGLSPTVWLSYIMMMYWGPSLYSLSPF 267

QY 181 SPLLPFFC 189
DB SPLLPFFC 276

RESULT 15

ADG76901 standard; protein; 309 AA.

ID ADG76901;

DT 11-MAR-2004 (first entry)

DE Hepatitis B virus envelope amino acid sequence SegID24.

KM hepatitis B virus; HBV; polymerase; ADV; LMV; TVF; FIC; ADV; LMV; ADV;

KM TVF; anti-HBV agent; hepatotropic; virucide; antiinflammatory;
KM HBV variant polymerase-antagonist; gene therapy; viral component;
KM inhibiting infection; virus replication; virus release; envelope.

OS Hepatitis B virus.

XX WO2003087351-A1.

PD 23-OCT-2003.

PF 11-APR-2003; 2003WO-AU000432.

PR 12-APR-2002; 2002AU-00001710.

PR 26-JUN-2002; 2002AU-00003224.

PA (MELB-) MELBOURNE HEALTH
(AUST-) AUSTIN & REPAIRATION MEDICAL CENT.
(SHEA-) SOUTHERN HEALTH.

PI Barcholemeuz AI, Locarnini SA, Ayres A, Colledge D, Sasadenuez J,
PI Tillmann H, Angus PM, Stevert W;

DR WPI; 2003-845324/78.

PT New isolated hepatitis B viral variants with reduced susceptibility to
PT nucleoside analogs, useful for screening, designing and/or developing
PT agents capable of inhibiting infection, replication and/or release of the
PT virus.

PS Example 5; SEQ ID NO 24; 268bp; English.

CC This invention relates to a novel isolated hepatitis B virus (HBV)

CC variant which comprises a nucleoside mutation in a gene encoding a DNA
CC polymerase resulting in at least one amino acid addition, substitution
CC and/or deletion to the polymerase, and exhibiting decreased sensitivity
CC to (for example) ADV, LMV, TVF, or FIC, or ADV and LMV, ADV and TVF,
CC and/or other nucleoside, analogues, anti-HBV agents or their
CC combinations. The invention may be useful for the development of
CC compounds with a hepatotropic, virucide or antiinflammatory activity as
CC HBV variant polymerase-antagonists. In addition, the sequences may be
CC useful for gene therapy. The HBV variants or their component are useful
CC in the rational design of an anti-HBV agent comprising microarray
CC analysis and is based on the crystal structure or NMR structure of a
CC viral component. The methods and compositions of the present invention
CC are also useful for screening, designing and/or developing agents capable
CC of inhibiting infection, replication and/or release of the virus.

XX Sequence 309 AA;

Query Match 95.9%; Score 1040; DB 7; Length 309;

Best Local Similarity 95.8%; Pred. No. 3.2e-86; Indels 0; Gaps 0;

Matches 181; Conservative 2; Mismatches 6;

QY 1 DSMWTSINFLGGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCL 60
DB DSMWTSINFLGGTTVCLGQNSQSPTSNHSPTSCPTCPGKRWMLRRFIIFILLCL 175

QY 61 FLVVLDDYQGLPVCPLIPGSSITTSKQCRCTCTPAQGTSMYPSCCCTPSPDNCICPI 120
DB FLVVLDDYQGLPVCPLIPGSSITTSKQCRCTCTPAQGTSMYPSCCCTPSPDNCICPI 235

QY 121 PSSMAFGKYLMEWASARFSWLSLVFPVQWFGLSPTVWLSYIMMMYWGPSLYSLSPF 180
DB PSSMAFGKYLMEWASARFSWLSLVFPVQWFGLSPTVWLSYIMMMYWGPSLYSLSPF 295

QY 181 SPLLPFFC 189
DB SPLLPFFC 304

Search completed: July 25, 2005, 11:21:29
Job time : 166 secs

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3M protein - protein search, using SW model

Run on: July 25, 2005, 11:13:41 / Search time 39 Seconds
(without alignments)
466.281 Million cell updates/sec

Title: US-09-823-077C-7
Perfect score: 1085
Sequence: 1 DSWMTSLNPLGTTVCIGQON.....GPSLYSLSPSPPLPIFFC 189

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1054	97.1	226	1 JQ1571	major surface anti
2	1054	97.1	389	1 SAVLHV	large surface anti
3	1054	97.1	389	1 S20745	surface antigen -
4	1054	97.1	389	2 S20753	surface antigen -
5	1050	96.8	226	2 JQ2077	surface antigen -
6	1050	96.8	226	2 JQ2076	surface antigen -
7	1049	96.7	226	2 JQ2078	surface antigen -
8	1047	96.5	226	2 JQ2079	surface antigen -
9	1046	96.4	226	2 JQ2075	surface antigen -
10	1046	96.4	226	2 JQ2073	surface antigen -
11	1046	96.4	389	2 S32202	large surface anti
12	1044	96.2	226	2 JQ2069	surface antigen -
13	1043	96.1	226	2 JQ2081	surface antigen -
14	1041	95.9	389	1 S47407	surface antigen -
15	1040	95.9	226	1 JQ1572	major surface anti
16	1040	95.9	226	2 JQ2065	surface antigen -
17	1040	95.9	226	2 JQ2067	surface antigen -
18	1040	95.9	226	2 JQ2083	surface antigen -
19	1040	95.9	389	1 SAVLHV	large surface anti
20	1037	95.6	226	2 JQ2066	surface antigen -
21	1037	95.6	226	2 JQ2063	surface antigen -
22	1037	95.6	389	1 SAVLHV	large surface anti
23	1037	95.6	389	1 SAVLHV	large surface anti
24	1036	95.5	226	2 JQ2068	surface antigen -
25	1031	95.0	226	2 JQ2070	surface antigen -
26	1030	94.9	226	2 JQ2080	surface antigen -
27	1027	94.7	226	2 JQ2072	surface antigen -
28	1017	93.7	226	2 JQ2050	surface antigen -
29	1016	93.6	226	2 JQ2092	surface antigen -

30	1012	93.3	226	2 JQ2085	surface antigen -
31	1010	93.1	226	2 JQ2054	surface antigen -
32	1007	92.8	226	1 JQ1573	major surface anti
33	1007	92.8	226	2 JQ2052	surface antigen -
34	1007	92.8	226	2 JQ2055	surface antigen -
35	1007	92.8	226	2 JQ2045	surface antigen -
36	1007	92.8	389	2 S41871	surface antigen -
37	1007	92.8	400	1 JQ1575	major surface anti
38	1007	92.8	400	1 SAVLHV	large surface anti
39	1006	92.7	226	2 JQ2087	surface antigen -
40	1006	92.7	226	2 JQ2089	surface antigen -
41	1006	92.7	226	2 JQ2090	surface antigen -
42	1006	92.7	226	2 JQ2091	surface antigen -
43	1005	92.6	226	1 JQ1577	major surface anti
44	1005	92.6	226	1 JQ1578	major surface anti
45	1004	92.5	226	1 SAVLHV	major surface anti

ALIGNMENTS

RESULT 1

JQ1571
Major surface antigen - hepatitis B virus (subtype ayw2)

C/Species: hepatitis B virus, HBV
A/Note: host Homo sapiens (man)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: JQ1571; JQ2074

R/Norder, H.; Hammas, B.; Loeferl, S.; Courouce, A.M.; Magnus, L.O.
U. Gen. Virol. 73, 1201-1208, 1992

A/Title: Comparison of the amino acid sequences of nine different serotypes of hepatitis
A/Reference number: JQ1570; PMID:92268879; PMID:15883323

A/Accession: JQ1571
A/Molecule type: DNA

A/Residues: 1-226 <NO2>
A/Cross-References: UNIPROT:Q69601; GB:X75662; NID:G416086; PIDN:CAA53349.1; PID:G416087

A/Experimental source: subtype ayw2, strain P2
J. Norder, H.; Hammas, B.; Lee, S.D.; Bille, K.; Courouce, A.M.; Mushahwar, I.K.; Magnus, L.O.
U. Gen. Virol. 74, 1341-1348, 1993

A/Title: Genetic relatedness of hepatitis B viral strains of diverse geographical origin
A/Reference number: JQ2044; PMID:93329382; PMID:8336122

A/Contents: genogroup D
A/Accession: JQ2074

A/Molecule type: DNA
A/Residues: 1-226 <NO2>

A/Experimental source: subtype ayw2, strain Ren
C/Genetics:

A/Gene: S
C/Superfamily: hepatitis B virus surface antigen

C/Keywords: glycoprotein; surface antigen
F.3/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.1% Score 1054; DB 1; Length 226;
Best Local Similarity 96.8%; Pred. No. 2.5e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY	1	DSWMTSLNPLGTTVCIGQONSPPTNSHSPSCPTCGGYRMCLRRFTIFPIILLICI	60
DB	33	DSWMTSLNPLGTTVCIGQONSPPTNSHSPSCPTCGGYRMCLRRFTIFPIILLICI	92
QY	61	FLVVLDDYQGLIPVCPILPGSSSTTSKQCRCTTTPAOGTSMYPSCCCTPSPDGNCTCIP1	120
DB	93	FLVVLDDYQGLIPVCPILPGSSSTTSKQCRCTTTPAOGTSMYPSCCCTPSPDGNCTCIP1	152
QY	121	PSWNAFGKYLWEMASARFSWLSLVPVQWFGVLSPTWLSVTMMWTGSPSLYSILSPF	180
DB	153	PSWNAFGKYLWEMASARFSWLSLVPVQWFGVLSPTWLSVTMMWTGSPSLYSILSPF	212
QY	181	SPILPIFFC 189	
DB	213	SPILPIFFC 221	

RESULT 2

SAVLBH

Large surface antigen - hepatitis B virus (subtype ayw, strain PHB320)
N/Contains: major surface antigen; middle surface antigen
C/Species: hepatitis B virus, HBV
A/Note: Host Homo sapiens (man)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A03704, P00585
R/Bichko, V.; Pushko, P.; Drellina, D.; Pumpen, P.; Gren, E.
FEBS Lett. 185, 208-212, 1985

A/Title: Subtype ayw variant of hepatitis B virus: DNA primary structure analysis.
A/Reference number: A05237; MID:85204397; PMID:3996597
A/Accession type: DNA
A/Molecule type: A03704
A/Residues: 1-389 <BIC>
A/Cross-references: UNIPROT:Q9WJ04; GB:X02496; NID:g62280; PIDD:CAH41701.1; PID:g4704321

R/Order: H.; Courouce, A.M.; Magnius, L.O.
U. Gen. Virol. 73, 3141-3145, 1992
A/Title: Molecular basis of hepatitis B virus serotype variations within the four major
A/Reference number: P00453; MID:93107848; PMID:1469353
A/Accession: P00585
A/Molecule type: DNA
A/Residues: 264-343 <NOR>
A/Experimental source: subtype ayw2, Tav

C/Genetics:
A/Gene: pre-S1/pre-S2/S
C/Superfamily: hepatitis B virus surface antigen
C/Keywords: glycoprotein, surface antigen
F/109-389/Product: middle surface antigen (gene pre-S2/S) #status predicted <DSA>
F/164-389/Product: major surface antigen (gene S) #status predicted <MSA>
F/164-112,166/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 97.1%; Score 1054; DB 1; Length 389;
Best Local Similarity 96.8%; Pred. No. 3.8e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 DSWMTSLNPLGTTVCLGQNSQSPHSPTSCPTCPGKRWMCRLRRFIIFLLILCL 60
Db 196 DSWMTSLNPLGTTVCLGQNSQSPHSPTSCPTCPGKRWMCRLRRFIIFLLILCL 255
Qy 61 FLVLVDYQGLIPVCPPIPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDGNCTCPI 120
Db 256 FLVLVDYQGLIPVCPPIPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDGNCTCPI 315
Qy 121 PSSMAFGKYLWEMASARFWSLSLVFPVQMFGLSPTVWLSVIMMMYWGSPSLYSILSPF 180
Db 316 PSSMAFGKYLWEMASARFWSLSLVFPVQMFGLSPTVWLSVIMMMYWGSPSLYSILSPF 375
Qy 181 SPLLPFPFC 189
Db 376 SPLLPFPFC 384
```

RESULT 3

S20745

surface antigen - hepatitis B virus (subtype ayw, patient C)
N/Alternate names: Hbs antigen
N/Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mid

C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, patient C
C/Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S20745
R/Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Wells, A.; Porru, A.
submitted to the EMBL Data Library, March 1992

A/Description: Sequence analysis of HBV genomes isolated from patients with HbsAg negat
A/Reference number: S20745
A/Accession: S20745
A/Molecule type: DNA
A/Residues: 1-389 <LAI>

A/Cross-references: UNIPROT:Q67871; EMBL:X65257; NID:g59429; PIDD:CAA46349.1; PID:g59430
A/Experimental source: subtype ayw, patient C
C/Genetics:
A/Gene: S

C/Superfamily: hepatitis B virus surface antigen

C/Keywords: surface antigen
F/1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS
F/1-108/Domain: pre-S1 domain #status predicted <PRE1>
F/109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted
F/109-163/Domain: pre-S2 domain #status predicted <PRE2>
F/164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 97.1%; Score 1054; DB 2; Length 389;
Best Local Similarity 96.8%; Pred. No. 3.8e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy 1 DSWMTSLNPLGTTVCLGQNSQSPHSPTSCPTCPGKRWMCRLRRFIIFLLILCL 60
Db 196 DSWMTSLNPLGTTVCLGQNSQSPHSPTSCPTCPGKRWMCRLRRFIIFLLILCL 255
Qy 61 FLVLVDYQGLIPVCPPIPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDGNCTCPI 120
Db 256 FLVLVDYQGLIPVCPPIPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDGNCTCPI 315
Qy 121 PSSMAFGKYLWEMASARFWSLSLVFPVQMFGLSPTVWLSVIMMMYWGSPSLYSILSPF 180
Db 316 PSSMAFGKYLWEMASARFWSLSLVFPVQMFGLSPTVWLSVIMMMYWGSPSLYSILSPF 375
Qy 181 SPLLPFPFC 189
Db 376 SPLLPFPFC 384
```

RESULT 4

S20753

surface antigen - hepatitis B virus (subtype ayw, patient E)

N/Alternate names: envelope protein, Hbs antigen
N/Contains: surface antigen pre-S1 (large envelope protein); surface antigen pre-S2 (mi
C/Species: hepatitis B virus, HBV
A/Variety: subtype ayw, patient E

C/Date: 20-Feb-1995 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: S20753
R/Lai, M.E.; Mazzoleni, A.P.; Balestrieri, A.; Wells, A.; Porru, A.
submitted to the EMBL Data Library, March 1992

A/Description: Sequence analysis of HBV genomes isolated from patients with HbsAg negat
A/Reference number: S20745
A/Accession: S20753
A/Molecule type: DNA
A/Residues: 1-389 <LAI>

A/Cross-references: UNIPROT:Q67879; EMBL:X65259; NID:g59439; PIDD:CAA46357.1; PID:g5944
A/Experimental source: subtype ayw, patient E
C/Genetics:
A/Gene: S

C/Superfamily: hepatitis B virus surface antigen

C/Keywords: surface antigen
F/1-389/Product: surface antigen pre-S1 (large envelope protein) #status predicted <PS1
F/1-108/Domain: pre-S1 domain #status predicted <PRE1>
F/109-389/Product: surface antigen pre-S2 (middle envelope protein) #status predicted
F/109-163/Domain: pre-S2 domain #status predicted <PRE2>
F/164-389/Product: surface antigen S (small envelope protein) #status predicted <PSD>

Query Match 97.1%; Score 1054; DB 2; Length 389;
Best Local Similarity 96.8%; Pred. No. 3.8e-77;
Matches 183; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

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Qy 1 DSWMTSLNPLGTTVCLGQNSQSPHSPTSCPTCPGKRWMCRLRRFIIFLLILCL 60
Db 196 DSWMTSLNPLGTTVCLGQNSQSPHSPTSCPTCPGKRWMCRLRRFIIFLLILCL 255
Qy 61 FLVLVDYQGLIPVCPPIPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDGNCTCPI 120
Db 256 FLVLVDYQGLIPVCPPIPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDGNCTCPI 315
Qy 121 PSSMAFGKYLWEMASARFWSLSLVFPVQMFGLSPTVWLSVIMMMYWGSPSLYSILSPF 180
Db 316 PSSMAFGKYLWEMASARFWSLSLVFPVQMFGLSPTVWLSVIMMMYWGSPSLYSILSPF 375
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186 DSMWTSIMFLGGTTCVCLGQNSQSPTSNHSPTSCPTPGVRMMLRRITIIFLFILLCLII 255

61 FLVLVLDYQGIIPVCEPLIPGSSFTTSKQCRTCTTPAAGTSNYPSCCCCKPNDGNCIPI 120

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 25, 2005, 11:15:11 / Search time 42 Seconds

(without alignments)
335,921 Million cell updates/sec

Title: US-09-823-077C-7

Perfect score: 1085
Sequence: 1 DSWMTSLNFGTTCVCLGQN.....GPSLSTLSPPSPPLPIFFC 189Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA.*
1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1040	95.9	226 4	US-10-104-966-10 Sequence 10, Appl
2	1040	95.9	249 4	US-09-311-784A-16 Sequence 16, Appl
3	1040	95.9	281 1	US-08-105-483-214 Sequence 214, App
4	1040	95.9	281 1	US-08-709-209-214 Sequence 214, App
5	1040	95.9	281 1	US-08-458-101-214 Sequence 214, App
6	1040	95.9	281 4	US-09-247-890-12 Sequence 12, Appl
7	1040	95.9	281 4	US-09-724-969-12 Sequence 12, Appl
8	1040	95.9	281 4	US-09-724-852-12 Sequence 12, Appl
9	1040	95.9	389 1	US-08-105-483-216 Sequence 216, App
10	1040	95.9	389 1	US-08-105-483-219 Sequence 219, App
11	1040	95.9	389 1	US-08-709-209-216 Sequence 216, App
12	1040	95.9	389 1	US-08-709-209-219 Sequence 219, App
13	1040	95.9	389 1	US-08-458-101-216 Sequence 216, App
14	1040	95.9	389 1	US-08-458-101-219 Sequence 219, App
15	1040	95.9	389 3	US-08-486-099-106 Sequence 106, App
16	1040	95.9	389 3	US-08-360-107A-116 Sequence 116, App
17	1040	95.9	389 3	US-08-484-233B-106 Sequence 106, App
18	1040	95.9	389 3	US-08-919-597-106 Sequence 106, App
19	1040	95.9	389 3	US-08-475-668A-106 Sequence 106, App
20	1040	95.9	389 3	US-08-485-551A-106 Sequence 106, App
21	1040	95.9	389 3	US-08-471-913A-106 Sequence 106, App
22	1040	95.9	389 3	US-08-485-264A-106 Sequence 106, App
23	1040	95.9	389 3	US-08-474-349A-106 Sequence 106, App
24	1040	95.9	389 4	US-08-470-896-106 Sequence 106, App
25	1040	95.9	389 4	US-08-485-546A-106 Sequence 106, App
26	1040	95.9	389 4	US-08-487-266A-106 Sequence 106, App
27	1040	95.9	397 5	PCT-US96-10602-6 Sequence 6, Appl

28	1033	95.2	226 5	PCT-US96-10602-14	Sequence 14, Appl
29	1007	92.8	225 6	5436139-4	Patent No. 5436139
30	1007	92.8	225 6	5436139-4	Patent No. 5436139
31	1007	92.8	226 6	5196194-21	Patent No. 5196194
32	1007	92.8	226 6	5436139-5	Patent No. 5436139
33	1007	92.8	226 6	5196194-21	Patent No. 5196194
34	1007	92.8	226 6	5436139-5	Patent No. 5436139
35	1007	92.8	281 4	US-09-721-480-3	Sequence 3, Appl
36	1007	92.8	390 4	US-09-721-480-5	Sequence 5, Appl
37	1007	92.8	531 4	US-09-721-480-7	Sequence 7, Appl
38	1004	92.5	387 4	US-09-350-841A-1592	Sequence 1592, Ap
39	1004	92.5	423 2	US-08-760-797A-1	Sequence 1, Appl
40	1004	92.5	424 2	US-08-760-797A-3	Sequence 3, Appl
41	1004	92.5	424 3	US-08-932-929B-1	Sequence 1, Appl
42	1004	92.5	424 3	US-08-932-929B-3	Sequence 3, Appl
43	995.5	91.8	395 6	5196194-18	Patent No. 5196194
44	995.5	91.8	395 6	5196194-18	Patent No. 5196194
45	992	91.4	226 1	US-08-378-011A-3	Sequence 3, Appl

ALIGNMENTS

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RESULT 1
US-10-104-966-10
Sequence 10, Application US/10104966
Patent No. 6680059
GENERAL INFORMATION:
APPLICANT: Marti Salberg
TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
FILE REFERENCE: TRIPEP.23AUSC1
CURRENT APPLICATION NUMBER: US/10/104,966
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/705,547
PRIOR FILING DATE: 2000-11-03
PRIOR APPLICATION NUMBER: 60/229,175
PRIOR FILING DATE: 2000-08-29
NUMBER OF SEQ ID NOS: 15
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10
LENGTH: 226
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Hepatitis B virus S antigen (HBeAg) sequence
US-10-104-966-10
Query Match 95.9%; Score 1040; DB 4; Length 226;
Best Local Similarity 95.8%; Pred. No. 7.7e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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2 11111111111111111111111111111111111111111111111111111
3 DSWMTSLNFGTTCVCLGQNSQSTSNHSPSCPTCPGRMCLRRPIIFLLICLI 92
4 11111111111111111111111111111111111111111111111111111
5 FLVLLDYOGILPYCPILPGSSSTSKGCRCTTPAOGTSMYPSGCCCKPSDGNCTCPI 120
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7 FLVLLDYOGILPYCPILPGSSSTSKGCRCTTPAOGTSMYPSGCCCKPSDGNCTCPI 152
8 11111111111111111111111111111111111111111111111111111
9 PPSNAFGKTYLWENASARFWSLVLVPVQWFGSLPTVWLSVIMWMYGBSLYSILSPF 180
10 11111111111111111111111111111111111111111111111111111
11 PPSNAFGKTYLWENASARFWSLVLVPVQWFGSLPTVWLSVIMWMYGBSLYSILSPF 212
12 11111111111111111111111111111111111111111111111111111
13 181 SPLPIFFC 189
14 11111111111111111111111111111111111111111111111111111
15 213 LPLPIFFC 221
16 11111111111111111111111111111111111111111111111111111
RESULT 2
US-09-311-784A-16
Sequence 16, Application US/09311784A
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Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Settle, Alessandro
APPLICANT: Ishioke, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: Epiimmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311.784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/086,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 249
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PADRE-HBV-s
US-09-311-784A-16

Query Match 95.9%; Score 1040; DB 4; Length 249;
Best Local Similarity 95.8%; Pred. No. 8.6e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNFGGTTVCIGGNSQSPSTNSHPTSCPTCPGRRMCLRRFIIFLLILCL1 60
DB 56 DSWMTSLNFGGTTVCIGGNSQSPSTNSHPTSCPTCPGRRMCLRRFIIFLLILCL1 115
QY 61 FLVLVDYQGLVPCPLIPSSSTTSKGQCRCTCTTAAQGTSMYPSCCCTKPSDGNCTCIP1 120
DB 116 FLVLVDYQGLVPCPLIPSSSTTSKGQCRCTCTTAAQGTSMYPSCCCTKPSDGNCTCIP1 175
QY 121 PSSWARGKYLMEWASAFWSLSLVPVQWFGVLSPTVMTSVTMMWYMGPSLYSILSPF 180
DB 176 PSSWARGKYLMEWASAFWSLSLVPVQWFGVLSPTVMTSVTMMWYMGPSLYSILSPF 235
QY 181 SPLPIFFC 189
DB 236 LPLPIFFC 244

RESULT 3
US-08-105-483-214
Sequence 214, Application US/08105483
Patent No. 5494807
GENERAL INFORMATION:
APPLICANT: Paolietti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483
FILING DATE: 12-AUG-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-214

Query Match 95.9%; Score 1040; DB 1; Length 281;
Best Local Similarity 95.8%; Pred. No. 9.8e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNFGGTTVCIGGNSQSPSTNSHPTSCPTCPGRRMCLRRFIIFLLILCL1 60
DB 88 DSWMTSLNFGGTTVCIGGNSQSPSTNSHPTSCPTCPGRRMCLRRFIIFLLILCL1 147
QY 61 FLVLVDYQGLVPCPLIPSSSTTSKGQCRCTCTTAAQGTSMYPSCCCTKPSDGNCTCIP1 120
DB 148 FLVLVDYQGLVPCPLIPSSSTTSKGQCRCTCTTAAQGTSMYPSCCCTKPSDGNCTCIP1 207
QY 121 PSSWARGKYLMEWASAFWSLSLVPVQWFGVLSPTVMTSVTMMWYMGPSLYSILSPF 180
DB 208 PSSWARGKYLMEWASAFWSLSLVPVQWFGVLSPTVMTSVTMMWYMGPSLYSILSPF 267
QY 181 SPLPIFFC 189
DB 268 LPLPIFFC 276

RESULT 4
US-08-709-209-214
Sequence 214, Application US/08709209
Patent No. 5762938
GENERAL INFORMATION:
APPLICANT: Paolietti, Enzo
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209
FILING DATE: 21-AUG-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483
FILING DATE: 12-AUG-1993
APPLICATION NUMBER: US 07/847,951
FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-709-209-214

Query Match 95.9%; Score 1040; DB 1; Length 281;
Best Local Similarity 95.8%; Pred. No. 9.8e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLGAGTTCVCGNSQSPSTNSHSPSCPTCGYRMCLRRPIIFLFIILLCI 60
DB 88 DSWMTSLNPLGAGTTCVCGNSQSPSTNSHSPSCPTCGYRMCLRRPIIFLFIILLCI 147
QY 61 FLVLVDYQGLPVCPLIPGSSSTTSKQCRCTTTPAQTSMYPSCCCTKPSDGNCTCPI 120
DB 148 FLVLVDYQGLPVCPLIPGSSSTTSKQCRCTTTPAQTSMYPSCCCTKPSDGNCTCPI 207
QY 121 PSSWAFKRTIEMWASARFWSLSLVFVQWFGVLSPTVWLSVIMMTWGPSLSYLSLSPF 180
DB 208 PSSWAFKRTIEMWASARFWSLSLVFVQWFGVLSPTVWLSVIMMTWGPSLSYLSLSPF 267
QY 181 SPLPIFFC 189
DB 268 LPLPIFFC 276

RESULT 5

US-08-458-101-214
Sequence 214, Application US/08458101
Patent No. 5766599
GENERAL INFORMATION:
APPLICANT: Paolletti, Enzo
APPLICANT: Perkus, Marlon E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: No. 5766599, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettis, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 214:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-214

Query Match 95.9%; Score 1040; DB 1; Length 281;
Best Local Similarity 95.8%; Pred. No. 9.8e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLGAGTTCVCGNSQSPSTNSHSPSCPTCGYRMCLRRPIIFLFIILLCI 60
DB 88 DSWMTSLNPLGAGTTCVCGNSQSPSTNSHSPSCPTCGYRMCLRRPIIFLFIILLCI 147
QY 61 FLVLVDYQGLPVCPLIPGSSSTTSKQCRCTTTPAQTSMYPSCCCTKPSDGNCTCPI 120
DB 148 FLVLVDYQGLPVCPLIPGSSSTTSKQCRCTTTPAQTSMYPSCCCTKPSDGNCTCPI 207
QY 121 PSSWAFKRTIEMWASARFWSLSLVFVQWFGVLSPTVWLSVIMMTWGPSLSYLSLSPF 180
DB 208 PSSWAFKRTIEMWASARFWSLSLVFVQWFGVLSPTVWLSVIMMTWGPSLSYLSLSPF 267
QY 181 SPLPIFFC 189
DB 268 LPLPIFFC 276

RESULT 6

US-09-247-890-12
Sequence 12, Application US/09247890
Patent No. 654101
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Baas, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, William P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT FILING DATE: 1999-02-10
EARLIER FILING DATE: 1998-02-11
EARLIER APPLICATION NUMBER: US 60/105,509
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 12
LENGTH: 281
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-247-890-12

Query Match 95.9%; Score 1040; DB 4; Length 281;
Best Local Similarity 95.8%; Pred. No. 9.8e-89;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLGAGTTCVCGNSQSPSTNSHSPSCPTCGYRMCLRRPIIFLFIILLCI 60
DB 88 DSWMTSLNPLGAGTTCVCGNSQSPSTNSHSPSCPTCGYRMCLRRPIIFLFIILLCI 147
QY 61 FLVLVDYQGLPVCPLIPGSSSTTSKQCRCTTTPAQTSMYPSCCCTKPSDGNCTCPI 120
DB 148 FLVLVDYQGLPVCPLIPGSSSTTSKQCRCTTTPAQTSMYPSCCCTKPSDGNCTCPI 207

Qy	121	PSSMAAGKTLMEASARFPMISLVPVQMFGSLSPYVLMSIVMMMYMGSLYSILSPF	189
		:	
Dδ	208	PSSMAAGKFLMEASARSFMSLSLVPVQMFGSLPTVMSIVMMMYMGSLYSILSPF	267
Qy	181	SPLLPFFC	189
Dδ	268	LPLPPLFFC	276

RESULT 7
US-09-724-969-12
; Sequence 12, Application US/09724965

```

1  GENERAL INFORMATION:
2  APPLICANT: Punnonen, Juhna
3  APPLICANT: Baas, Steven H.
4  APPLICANT: Whalen, Robert Gerald
5  APPLICANT: Howard, Russell
6  APPLICANT: Stemmer, Willem P. C.
7  APPLICANT: Maxygen, Inc.
8  TITLE OF INVENTION: Antigen Library Immunization
9  FILE REFERENCE: 018097-02871005
10 CURRENT APPLICATION NUMBER: US/09/724,969
11 CURRENT FILING DATE: 2000-11-28
12 PRIOR APPLICATION NUMBER: 09/247,690
13 PRIOR FILING DATE: 1999-02-10
14 PRIOR APPLICATION NUMBER: US 60/105,509
15 PRIOR FILING DATE: 1998-10-23
16 NUMBER OF SEQ ID NOS: 25
17 SOFTWARE: PatentIn Ver. 2.0
18 SEQ ID NO 12
19 LENGTH: 281
20 TYPE: PRN
21 ORGANISM: Hepatitis B virus
22 US-09-724-969-12

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Query Match	95.9%	Score 1040	DB 4	Length 281
Best Local Similarity	95.8%	Pred. No. 9	8e-89	
Matches 181	Conservative 2	Mismatches 6	Indels 0	Gaps 0
QY	1	DSWMTSLNFIAGGTTTCAGCNSQSPSTNHSPTSCPTCPGYRMWCLRRFTIIFLFIILLCI	60	
Db	88	DSWMTSLNFIAGGTTTCAGCNSQSPSTNHSPTSCPTCPGYRMWCLRRFTIIFLFIILLCI	147	
QY	61	FLVLVLDVQGLIPVCELI PGSSSTTSKGCCRTCTTFAOGSMWPSGCCCTKPSGNCCTCPI	120	
Db	148	FLVLVLDVQGLIPVCELI PGSSSTTSKGCCRTCTTFAOGSMWPSGCCCTKPSGNCCTCPI	207	
QY	121	PSSNAFGKYLIMENASARPSTLSLTPVQVFGVLSPTVWLSYIMMMWYGPGLYSILSBP	180	
Db	208	PSSNAFGKYLIMENASARPSTLSLTPVQVFGVLSPTVWLSYIMMMWYGPGLYSILSBP	267	
QY	181	SPLLPIPPC 189		
Db	268	LPLLPPIPPC 276		

RESULT 8
US-09-724-852-12
Sequence 12, Application US/09724852
Patent No. 6576757
GENERAL INFORMATION:
APPLICANT: Punnonen, Juha
APPLICANT: Baas, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Award, Russell
APPLICANT: Stemmer, Willem P. C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: AntiGen Library Immunizations
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/724,852
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US/09/247,890

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/ PRIOR FILING DATE: 1999-02-10 APPLICATION NUMBER: US 60/074,299
/ PRIOR APPLICATION NUMBER: EARLIER FILING DATE: 1998-02-11
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
/ PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,506
/ PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: Patencin Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 281
/ TYPE: PRF
/ ORGANISM: Hepatitis B virus
/ US-09-724-852-12

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	Query Match Similarity	95.9%	Score 1040;	DB 4;	Length 281;
	Best Local Similarity	95.8%	Pred. No. 9.8e-89;		
	Matches 101;	Conservative 2;	Mismatches 6;	Indels 0;	Gaps 0
QY	1	DSWMTSLNPLGGTTCGACGNSQSPTSNHSPSCPTCPGGRMNCLERFIIFELFILLCIL	60		
Db	88	DSWMTSLNPLFGGTTTCGACGNSQSPTSNHSPPSCPTCPGGRMNCLERFIIFELFILLCIL	147		
QY	61	FLTVLTDYQGLIVPVCPLPGSSTTSKQCCRTCTPAQGTMYRSCCTKPSDGNCTCFI	120		
Db	148	FLTVLTDYQGLIVPVCPLPGSSTTSKQCCRTCTPAQGTMYRSCCTKPSDGNCTCFI	207		
QY	121	PSSMAFGKILWEMASARFSWLSLVPVQVFGISPTVWLVIWMWYQPSLYSILSP	180		
Db	208	PSSMAFGKILWEMASARFSWLSLVPVQVFGISPTVWLVIWMWYQPSLYSILSP	267		
QY	181	SPLPLPFC	189		
Db	268	SPLPLPFC	276		

RESULT 9
 Sequence 216, Application US/08105483
 Patent No. 5494807
 GENERAL INFORMATION:
 APPLICANT: Paolletti, Enzo
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 TITLE OR INVENTION: STRAIN
 NUMBER OF SEQUENCES: 462
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Curtiss, Morris & Safford
 ADDRESSEE: c/o William S. Frommer
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/105,483
 FILING DATE: 12-AUG-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/847,951
 FILING DATE: 06-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2400
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 216:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-105-483-216

Query Match 95.9%; Score 1040; DB 1; Length 389;
Best Local Similarity 95.8%; Pred. No. 1.4e-88;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLGTTTCGONSGPTSNHSPSCPTCGYRMCLRRPIIFLLICLI 60
DB DSWMTSLNPLGTTTCGONSGPTSNHSPSCPTCGYRMCLRRPIIFLLICLI 255
QY 61 FLVLLDYQGLIPVCPPIPGSSTTSKQCRCTTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
DB FLVLLDYQGLIPVCPPIPGSSTTSKQCRCTTTPAOGTSMYPSCCCTKPSDGNCTCIP 315
QY 121 PSSWAFGKYLWEMASARFSLVLPVQWFGVLSPTVWLSVIMMYWGPSTLYSISPF 180
DB PSSWAFGKYLWEMASARFSLVLPVQWFGVLSPTVWLSVIMMYWGPSTLYSISPF 375
QY 181 SPLPIFFC 189
DB SPLPIFFC 384

RESULT 10

US-08-105-483-219
Sequence 219, Application US/08105483
Patent No. 5494807

GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford

ADDRESSER: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,483

FILING DATE: 12-AUG-1993
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 219:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-105-483-219

Query Match 95.9%; Score 1040; DB 1; Length 389;
Best Local Similarity 95.8%; Pred. No. 1.4e-88;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLGTTTCGONSGPTSNHSPSCPTCGYRMCLRRPIIFLLICLI 60
DB DSWMTSLNPLGTTTCGONSGPTSNHSPSCPTCGYRMCLRRPIIFLLICLI 255
QY 61 FLVLLDYQGLIPVCPPIPGSSTTSKQCRCTTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
DB FLVLLDYQGLIPVCPPIPGSSTTSKQCRCTTTPAOGTSMYPSCCCTKPSDGNCTCIP 315
QY 121 PSSWAFGKYLWEMASARFSLVLPVQWFGVLSPTVWLSVIMMYWGPSTLYSISPF 180
DB PSSWAFGKYLWEMASARFSLVLPVQWFGVLSPTVWLSVIMMYWGPSTLYSISPF 375
QY 181 SPLPIFFC 189
DB SPLPIFFC 384

RESULT 11

US-08-709-209-216
Sequence 216, Application US/08709209
Patent No. 5762938

GENERAL INFORMATION:
APPLICANT: Paoletti, Enzo

TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford

ADDRESSER: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York

STATE: NY
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/709,209

FILING DATE: 21-AUG-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/105,483

FILING DATE: 12-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 216:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids

TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-709-209-216

Query Match 95.9%; Score 1040; DB 1; Length 389;
Best Local Similarity 95.8%; Pred. No. 1.4e-88;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 DSWMTSLNPLGTTTCGONSGPTSNHSPSCPTCGYRMCLRRPIIFLLICLI 60
DB DSWMTSLNPLGTTTCGONSGPTSNHSPSCPTCGYRMCLRRPIIFLLICLI 255
QY 61 FLVLLDYQGLIPVCPPIPGSSTTSKQCRCTTTPAOGTSMYPSCCCTKPSDGNCTCIP 120
DB FLVLLDYQGLIPVCPPIPGSSTTSKQCRCTTTPAOGTSMYPSCCCTKPSDGNCTCIP 315
QY 121 PSSWAFGKYLWEMASARFSLVLPVQWFGVLSPTVWLSVIMMYWGPSTLYSISPF 180
DB PSSWAFGKYLWEMASARFSLVLPVQWFGVLSPTVWLSVIMMYWGPSTLYSISPF 375
QY 181 SPLPIFFC 189
DB SPLPIFFC 384

Db 256 FLVLLVDYQGLPVCLIPGSSSTTSGPCRTCTMTAGSMTYSCCCTKPSDNCCTCIP 315
 QY 121 PSSMAFGKTLMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMYMGPSLYSLSP 180
 316 PSSMAFGKTLMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMYMGPSLYSLSP 375
 Db 181 SPLPTFFC 189
 376 LPPLPTFFC 384

RESULT 12
 US-08-709-209-219
 / Sequence 219, Application US/08709209
 / Patent No. 5762938
 / GENERAL INFORMATION:
 / APPLICANT: Paoletti, Enzo
 / TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 / NUMBER OF SEQUENCES: 462
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Curtis, Morris & Safford
 / ADDRESSEE: c/o William S. Frommer
 / STREET: 530 Fifth Avenue
 / CITY: New York
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10036
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/709,209
 / FILING DATE: 21-AUG-1996
 / CLASSIFICATION: 424
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: US 08/105,483
 / FILING DATE: 12-AUG-1993
 / APPLICATION NUMBER: US 07/847,951
 / FILING DATE: 06-MAR-1992
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Frommer, William S.
 / REGISTRATION NUMBER: 25,506
 / REFERENCE/DOCKET NUMBER: 454310-2400
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212) 840-3333
 / TELEFAX: (212) 840-0712
 / INFORMATION FOR SEQ ID NO: 219:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 389 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-709-209-219

Query Match 95.9%; Score 1040; DB 1; Length 389;
 Best Local Similarity 95.8%; Pred. No. 1.4e-88;
 Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DSWMTSLNFIAGGTVCLIGNSQSPSTNSHPTSCPTCPGYRMWCLRRFIIFLFIILLCI 60
 Db 196 DSWMTSLNFIAGGTVCLIGNSQSPSTNSHPTSCPTCPGYRMWCLRRFIIFLFIILLCI 255
 QY 61 FLVLLVDYQGLPVCLIPGSSSTTSKGCCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 120
 Db 256 FLVLLVDYQGLPVCLIPGSSSTTSKGCCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 315
 QY 121 PSSMAFGKTLMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMYMGPSLYSLSP 180
 Db 316 PSSMAFGKTLMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMYMGPSLYSLSP 375

QY 181 SPLPTFFC 189
 Db 376 LPPLPTFFC 384

RESULT 13
 US-08-458-101-216
 / Sequence 216, Application US/08458101
 / Patent No. 5765599
 / GENERAL INFORMATION:
 / APPLICANT: Paoletti, Enzo
 / APPLICANT: Perkus, Marion B.
 / APPLICANT: Taylor, Jill
 / APPLICANT: Tartaglia, James
 / APPLICANT: No. 5765599con, Elizabeth K.
 / APPLICANT: Riviere, Michel
 / APPLICANT: de Taisne, Charles
 / APPLICANT: Limbach, Keith J.
 / APPLICANT: Johnson, Gerard P.
 / APPLICANT: Pincus, Steven B.
 / APPLICANT: Cox, William I.
 / APPLICANT: Audomnet, Jean-Christophe Francis
 / APPLICANT: Gettig, Russell Robert
 / TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 / NUMBER OF SEQUENCES: 467
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Curtis, Morris & Safford
 / ADDRESSEE: c/o William S. Frommer
 / STREET: 530 Fifth Avenue
 / CITY: New York
 / STATE: NY
 / COUNTRY: USA
 / ZIP: 10036
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / OPERATING SYSTEM: IBM PC compatible
 / SOFTWARE: Patentin Release #1.0, Version #1.25
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/458,101
 / FILING DATE: 01-JUN-1995
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Frommer, William S.
 / REGISTRATION NUMBER: 25,506
 / REFERENCE/DOCKET NUMBER: 454310-2740
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212) 840-3333
 / TELEFAX: (212) 840-0712
 / INFORMATION FOR SEQ ID NO: 216:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 389 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / US-08-458-101-216

Query Match 95.9%; Score 1040; DB 1; Length 389;
 Best Local Similarity 95.8%; Pred. No. 1.4e-88;
 Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DSWMTSLNFIAGGTVCLIGNSQSPSTNSHPTSCPTCPGYRMWCLRRFIIFLFIILLCI 60
 Db 196 DSWMTSLNFIAGGTVCLIGNSQSPSTNSHPTSCPTCPGYRMWCLRRFIIFLFIILLCI 255
 QY 61 FLVLLVDYQGLPVCLIPGSSSTTSKGCCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 120
 Db 256 FLVLLVDYQGLPVCLIPGSSSTTSKGCCTCTTPAOGTSMYPSCCCTKPSDNCCTCIP 315
 QY 121 PSSMAFGKTLMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMYMGPSLYSLSP 180

316 PSSNAFGKXLMENASAFBSWLSLVFVQWFGLSPTVWLSVIMMMWGWGSLXSLSPF 375
 181 SPLLPFFC 189
 376 LPLLPFFC 384

RESULT 14
 US-08-458-101-219

Sequence 219, Application US/08458101
 Patent No. 576599

GENERAL INFORMATION:

APPLICANT: Paolucci, Enzo
 APPLICANT: Perkins, Marion E.
 APPLICANT: Taylor, Jill
 APPLICANT: Tartaglia, James
 APPLICANT: No. 576599, Elizabeth K.
 APPLICANT: Riviere, Michel
 APPLICANT: de Talsne, Charles
 APPLICANT: Lambach, Keith J.
 APPLICANT: Johnson, Gerard P.
 APPLICANT: Plucius, Steven E.
 APPLICANT: Cox, William I.
 APPLICANT: Audonnet, Jean-Christophe Francis
 TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
 TITLE OF INVENTION: STRAIN
 NUMBER OF SEQUENCES: 467
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Curtis, Morris & Safford
 ADDRESSEE: C/O William S. Frommer
 STREET: 530 Fifth Avenue
 CITY: New York
 STATE: NY
 COUNTRY: USA
 ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/458,101
 FILING DATE: 01-JUN-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2740
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 INFORMATION FOR SEQ ID NO: 219:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-458-101-219

Query Match 95.9%, Score 1040, DB 1, Length 389,
 Best Local Similarity 95.8%, Pred. No. 1.4e-88,
 Matches 181, Conservative 2, Mismatches 6, Indels 0, Gaps 0,

1 DSWTSLNPLGATTCVCLGNSOSPSTNSHPTSCPTCPGYRMWCLRRFIIFLLICLI 60
 196 DSWTSLNPLGATTCVCLGNSOSPSTNSHPTSCPTCPGYRMWCLRRFIIFLLICLI 255
 61 FLVTLVDYQGLPVCPLIPSSSTTSKQCRCTTPAOGTSMTPSCCTTSDGACTCIP 120
 256 FLVTLVDYQGLPVCPLIPSSSTTSKQCRCTTPAOGTSMTPSCCTTSDGACTCIP 315
 121 PSSNAFGKXLMENASAFBSWLSLVFVQWFGLSPTVWLSVIMMMWGWGSLXSLSPF 180

316 PSSNAFGKXLMENASAFBSWLSLVFVQWFGLSPTVWLSVIMMMWGWGSLXSLSPF 375
 181 SPLLPFFC 189
 376 LPLLPFFC 384

RESULT 15
 US-08-486-099-106

Sequence 106, Application US/08486099
 Patent No. 6013263

GENERAL INFORMATION:

APPLICANT: Bolognesi, Paul P.
 APPLICANT: Matthews, Thomas J.
 APPLICANT: Wild, Carl T.
 APPLICANT: Barney, Shawn O.
 APPLICANT: Lambert, Dennis M.
 APPLICANT: Peteway, Stephen R.
 APPLICANT: Langlois, Alphonse J.
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 NUMBER OF SEQUENCES: 209
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,099
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-031
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 INFORMATION FOR SEQ ID NO: 106:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 US-08-486-099-106

Query Match 95.9%, Score 1040, DB 3, Length 389,
 Best Local Similarity 95.8%, Pred. No. 1.4e-88,
 Matches 181, Conservative 2, Mismatches 6, Indels 0, Gaps 0,

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 196 DSWTSLNPLGATTCVCLGNSOSPSTNSHPTSCPTCPGYRMWCLRRFIIFLLICLI 255
 61 FLVTLVDYQGLPVCPLIPSSSTTSKQCRCTTPAOGTSMTPSCCTTSDGACTCIP 120
 256 FLVTLVDYQGLPVCPLIPSSSTTSKQCRCTTPAOGTSMTPSCCTTSDGACTCIP 315
 121 PSSNAFGKXLMENASAFBSWLSLVFVQWFGLSPTVWLSVIMMMWGWGSLXSLSPF 180
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GenCore version 5.1.6
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OM protein - protein search, using BW model

Run on: July 25, 2005, 11:24:37 / Search time 156 Seconds
(without alignments)
471.279 Million cell updates/sec

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Perfect score: 1085
Sequence: 1 DSWMTSLNPLGCTVCLGQN.....GPSLYSLSPSPPLPFFFC 189

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1046	96.4	226	US-10-169-668-5	Sequence 5, Appl
2	1046	96.4	389	US-10-169-668-6	Sequence 6, Appl
3	1043	96.1	226	US-10-911-464B-36	Sequence 36, Appl
4	1040	95.9	226	US-09-929-955-10	Sequence 10, Appl
5	1040	95.9	226	US-10-104-966-10	Sequence 10, Appl
6	1040	95.9	226	US-10-719-619-10	Sequence 10, Appl
7	1040	95.9	226	US-10-817-581-10	Sequence 10, Appl
8	1040	95.9	227	US-10-472-724-17	Sequence 10, Appl
9	1040	95.9	249	US-10-371-525-16	Sequence 16, Appl
10	1040	95.9	249	US-10-371-069-16	Sequence 16, Appl
11	1040	95.9	249	US-10-371-645-16	Sequence 16, Appl

12	1040	95.9	249	US-10-371-260-16	Sequence 16, Appl
13	1040	95.9	281	US-09-247-890-12	Sequence 12, Appl
14	1040	95.9	281	US-10-383-317-12	Sequence 12, Appl
15	1040	95.9	334	US-10-472-724-10	Sequence 10, Appl
16	1040	95.9	389	US-10-267-682-106	Sequence 106, App
17	1040	95.9	389	US-10-267-682-106	Sequence 106, App
18	1040	95.9	397	US-09-812-862-6	Sequence 6, Appl
19	1033	95.2	226	US-09-812-862-14	Sequence 14, Appl
20	1033	95.2	389	US-09-821-877-2	Sequence 2, Appl
21	1033	95.2	389	US-10-847-493-2	Sequence 2, Appl
22	1032	95.1	229	US-09-821-877-8	Sequence 8, Appl
23	1032	95.1	229	US-10-847-493-8	Sequence 8, Appl
24	1026	94.6	305	US-10-911-464B-30	Sequence 30, Appl
25	1007	92.8	226	US-10-838-834-14	Sequence 14, Appl
26	1007	92.8	281	US-10-715-665-3	Sequence 3, Appl
27	1007	92.8	390	US-10-715-665-5	Sequence 5, Appl
28	1007	92.8	454	US-10-912-869-38	Sequence 38, Appl
29	1007	92.8	531	US-10-715-665-7	Sequence 7, Appl
30	1007	92.8	678	US-10-365-620-29	Sequence 29, Appl
31	1007	92.8	678	US-10-365-620-32	Sequence 32, Appl
32	1007	92.8	678	US-10-912-969-36	Sequence 36, Appl
33	1007	92.8	678	US-10-913-171-29	Sequence 29, Appl
34	991	91.3	226	US-10-335-774-2	Sequence 2, Appl
35	991	91.3	226	US-10-335-774-40	Sequence 40, Appl
36	988	91.1	400	US-10-411-026-46	Sequence 46, Appl
37	988	91.1	400	US-10-411-026-46	Sequence 46, Appl
38	988	91.1	400	US-10-410-949-46	Sequence 46, Appl
39	988	91.1	400	US-10-410-949-46	Sequence 46, Appl
40	988	91.1	400	US-10-410-930-46	Sequence 46, Appl
41	988	91.1	400	US-10-410-997-46	Sequence 46, Appl
42	988	91.1	400	US-10-411-012-46	Sequence 46, Appl
43	988	91.1	400	US-10-287-994-46	Sequence 46, Appl
44	988	91.1	400	US-10-410-913-46	Sequence 46, Appl
45	988	91.1	400	US-10-410-980-46	Sequence 46, Appl

ALIGNMENTS

RESULT 1
US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIONEERIEUX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC AND PROTEIN
; FILE REFERENCE: IFR 99 INS HBV
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match	96.4%	Score 1046;	DB 14;	Length 226;
Beat Local Similarity	95.8%	Pred. No. 1.9e-82;		
Matches 181;	Conservative 3;	Mismatches 5;	Indels 0;	Gaps 0;
QY	1	DSWMTSLNPLGCTVCLGQNSQSPSTNSPTSCPTCGYMMCLRRIFILFLICLI	60	
DB	33	DSWMTSLNPLGCTVCLGQNSQSPSTNSPTSCPTCGYMMCLRRIFILFLICLI	92	
QY	61	FLVTLVDQGLPLPCPLPGSSTSKGQCRCTTTPAOSTSYRSCCCCKBBDGNTCPI	120	
DB	93	FLVTLVDQGLPLPCPLPGSSTSKGQCRCTTTPAOSTSYRSCCCCKBBDGNTCPI	152	
QY	121	PSNAFGKYLKEMASRPSMTSLVLPFQWFGVGLPTWLSVIMMMWTGSLYSISPF	180	

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: July 25, 2005, 11:24:37 ; Search time 156 Seconds

(without alignments)
471.279 Million cell updates/sec

Title: US-09-823-077C-7

Perfect score: 1085
Sequence: 1 DSMWTSINFLGAGTTVCAGQN.....GPSLXSLSPSPPLPIFC 189

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/1/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/1/pubppaa/US10F_PUBCOMB.pep.*
- 19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/1/pubppaa/US11A_PUBCOMB.pep.*
- 21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1046	96.4	226	14	US-10-169-668-5
2	1046	96.4	389	14	US-10-169-668-6
3	1043	96.1	226	18	US-10-911-4648-36
4	1040	95.9	226	9	US-09-929-955-10
5	1040	95.9	226	13	US-10-104-966-10
6	1040	95.9	226	15	US-10-719-619-10
7	1040	95.9	226	16	US-10-817-591-10
8	1040	95.9	227	16	US-10-472-724-27
9	1040	95.9	249	15	US-10-371-525-16
10	1040	95.9	249	15	US-10-371-069-16
11	1040	95.9	249	15	US-10-371-645-16

12	1040	95.9	249	15	US-10-371-260-16	Sequence 16, App1
13	1040	95.9	281	9	US-09-247-890-12	Sequence 12, App1
14	1040	95.9	281	15	US-10-363-317-12	Sequence 12, App1
15	1040	95.9	334	16	US-10-472-724-10	Sequence 10, App1
16	1040	95.9	389	15	US-10-267-682-106	Sequence 106, App
17	1040	95.9	389	15	US-10-267-748-106	Sequence 106, App
18	1040	95.9	397	9	US-09-812-862-6	Sequence 6, App1
19	1033	95.2	226	9	US-09-812-862-14	Sequence 14, App1
20	1033	95.2	389	16	US-09-821-877-2	Sequence 2, App1
21	1033	95.2	389	16	US-10-847-493-2	Sequence 2, App1
22	1032	95.1	229	9	US-09-821-877-8	Sequence 8, App1
23	1032	95.1	229	16	US-10-847-493-8	Sequence 8, App1
24	1026	94.6	305	18	US-10-911-4648-30	Sequence 30, App1
25	1007	92.8	226	17	US-10-838-834-14	Sequence 14, App1
26	1007	92.8	381	18	US-10-715-665-3	Sequence 3, App1
27	1007	92.8	390	18	US-10-715-665-5	Sequence 5, App1
28	1007	92.8	454	17	US-10-912-969-38	Sequence 38, App1
29	1007	92.8	531	18	US-10-715-665-7	Sequence 7, App1
30	1007	92.8	678	15	US-10-365-620-29	Sequence 29, App1
31	1007	92.8	678	15	US-10-365-620-32	Sequence 32, App1
32	1007	92.8	678	17	US-10-912-969-36	Sequence 36, App1
33	1007	92.8	678	17	US-10-913-171-29	Sequence 29, App1
34	991	91.3	226	15	US-10-335-774-2	Sequence 2, App1
35	991	91.3	226	15	US-10-335-774-40	Sequence 40, App1
36	988	91.1	400	15	US-10-411-037-46	Sequence 46, App1
37	988	91.1	400	15	US-10-411-026-46	Sequence 46, App1
38	988	91.1	400	15	US-10-410-962-46	Sequence 46, App1
39	988	91.1	400	15	US-10-411-049-46	Sequence 46, App1
40	988	91.1	400	16	US-10-410-930-46	Sequence 46, App1
41	988	91.1	400	16	US-10-410-997-46	Sequence 46, App1
42	988	91.1	400	16	US-10-411-012-46	Sequence 46, App1
43	988	91.1	400	16	US-10-287-994-46	Sequence 46, App1
44	988	91.1	400	16	US-10-410-913-46	Sequence 46, App1
45	988	91.1	400	17	US-10-410-980-46	Sequence 46, App1

ALIGNMENTS

RESULT 1

US-10-169-668-5
; Sequence 5, Application US/10169668
; Publication No. US20030129202A1
; GENERAL INFORMATION:
; APPLICANT: BIONEERIX
; APPLICANT: INSERM
; TITLE OF INVENTION: MUTATED HEPATITIS B VIRUS, ITS NUCLEIC ACID AND PROTEIN
; TITLE OF INVENTION: CONSTITUENTS AND USES THEREOF
; FILE REFERENCE: IFB 99 INS HBVM
; CURRENT APPLICATION NUMBER: US/10/169,668
; CURRENT FILING DATE: 2002-07-08
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: mutated hepatitis B virus mHBV
US-10-169-668-5

Query Match	96.4%	Score 1046;	DB 14;	Length 226;
Best Local Similarity	95.8%	Pred. No. 1.9e-82;		
Matches 181;	Conservative 3;	Mismatches 5;	Indels 0;	Gaps 0;
QY	1	DSMWTSINFLGAGTTVCAGQNSQSPSTNSHSPSCPTCGYRMCCIRPIIFLPIILLCLII	60	
DB	33	DSMWTSINFLGAGTTVCAGQNSQSPSTNSHSPSCPTCGYRMCCIRPIIFLPIILLCLII	92	
QY	61	FLVLIVDVGGLPVCPLPGSSSTSKGCCRCTTTPAOSTSMYPSGCCCKPBDGNTCTCPI	120	
DB	93	FLVLIVDVGGLPVCPLPGSSSTSKGCCRCTTTPAOSTSMYPSGCCCKPBDGNTCTCPI	152	
QY	121	PSNAFGKYLKEMASRSTSLVPPQVFGVSPVTWLSVIMMMYMGPSLYSLSPF	180	

Db 213 LPLPIRPEC 221

RESULT 5
US-10-104-966-10
Sequence 10, Application US/10104966
Publication No. US20020155124A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg
APPLICANT: Catharina Hultgren
TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TRIPEP.23AUSC1

CURRENT FILING DATE: 2002-03-22

PRIOR FILING DATE: 2000-11-03

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 226

TYPE: PRT

ORGANISM: Artificial Sequence

OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence

US-10-104-966-10

Query Match 95.9%; Score 1040; DB 13; Length 226;
Best Local Similarity 95.8%; Pred. No. 6.3e-82;

Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Db 1 DSMWTSINFLGCTTVCCLGQNSQSPSTNSHSPSCPTCGYRMCLRRPIIFILLCL 60

Db 3 DSMWTSINFLGCTTVCCLGQNSQSPSTNSHSPSCPTCGYRMCLRRPIIFILLCL 92

Db 61 FLVLLDYQGLPVCPPLPGSSTTSKQCRCTTTPAOGTSMYPSGCCCTKPSDGNCTCPI 120

Db 93 FLVLLDYQGLPVCPPLPGSSTTSKQCRCTTTPAOGTSMYPSGCCCTKPSDGNCTCPI 152

Db 121 PSSNAFGKYLMEWASARFSWLSLVFPVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 180

Db 153 PSSNAFGKYLMEWASARFSWLSLVFPVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 212

Qy 181 SPLPIRPEC 189

Db 213 LPLPIRPEC 221

RESULT 6
US-10-719-619-10Sequence 10, Application US/10719619
Publication No. US20040086529A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg
APPLICANT: Catharina Hultgren
TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TRIPEP.23AUSC1

CURRENT FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2000-11-03

PRIOR FILING DATE: 2000-08-29

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 226

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:
OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence

US-10-719-619-10

Query Match 95.9%; Score 1040; DB 15; Length 226;
Best Local Similarity 95.8%; Pred. No. 6.3e-82;

Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DSMWTSINFLGCTTVCCLGQNSQSPSTNSHSPSCPTCGYRMCLRRPIIFILLCL 60

Db 3 DSMWTSINFLGCTTVCCLGQNSQSPSTNSHSPSCPTCGYRMCLRRPIIFILLCL 92

Db 61 FLVLLDYQGLPVCPPLPGSSTTSKQCRCTTTPAOGTSMYPSGCCCTKPSDGNCTCPI 120

Db 93 FLVLLDYQGLPVCPPLPGSSTTSKQCRCTTTPAOGTSMYPSGCCCTKPSDGNCTCPI 152

Db 121 PSSNAFGKYLMEWASARFSWLSLVFPVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 180

Db 153 PSSNAFGKYLMEWASARFSWLSLVFPVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 212

Qy 181 SPLPIRPEC 189

Db 213 LPLPIRPEC 221

RESULT 7
US-10-817-591-10Sequence 10, Application US/10817591
Publication No. US20040229832A1

GENERAL INFORMATION:

APPLICANT: Matti Salberg
APPLICANT: Catharina Hultgren
TITLE OF INVENTION: VACCINES CONTAINING RIBAVIRIN AND
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: TRIPEP.23AUSC1

CURRENT FILING DATE: 2004-04-02

PRIOR FILING DATE: 2004-07-19, 619

PRIOR FILING DATE: 2003-11-20

PRIOR FILING DATE: 2002-03-22

PRIOR FILING DATE: 2001-08-15

PRIOR FILING DATE: 2000-08-29

PRIOR FILING DATE: 2000-08-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 10

LENGTH: 226

TYPE: PRT

ORGANISM: Artificial Sequence

OTHER INFORMATION: Hepatitis B virus S antigen (HBsAg) sequence

US-10-817-591-10

Query Match 95.9%; Score 1040; DB 16; Length 226;
Best Local Similarity 95.8%; Pred. No. 6.3e-82;

Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DSMWTSINFLGCTTVCCLGQNSQSPSTNSHSPSCPTCGYRMCLRRPIIFILLCL 60

Db 3 DSMWTSINFLGCTTVCCLGQNSQSPSTNSHSPSCPTCGYRMCLRRPIIFILLCL 92

Db 61 FLVLLDYQGLPVCPPLPGSSTTSKQCRCTTTPAOGTSMYPSGCCCTKPSDGNCTCPI 120

Db 93 FLVLLDYQGLPVCPPLPGSSTTSKQCRCTTTPAOGTSMYPSGCCCTKPSDGNCTCPI 152

Qy 121 PSSNAFGKYLMEWASARFSWLSLVFPVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 180

Db 153 PSSWAFGKFLWNASARFSLVLLVPFVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 212
Qy 181 SPLLPPIFFC 189
Db 213 LPLLPPIFFC 221

RESULT 8

US-10-472-724-27
; Sequence 27, Application US/10472724
; Publication No. US20040171806A1
; GENERAL INFORMATION:
; APPLICANT: Cid-Arregui, Angel
; APPLICANT: Zur Hausen, Harald
; TITLE OF INVENTION: Modified HPV E6 and E7 genes and proteins useful for vaccination
; FILE REFERENCE: 4121-154
; CURRENT APPLICATION NUMBER: US/10/472,724
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: PCT/EP02/03271
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: EP 01107271.7
; PRIOR FILING DATE: 2001-03-23
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 27
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic gene EHBs Ag-S-F
US-10-472-724-27

Query Match 95.9%; Score 1040; DB 16; Length 227;
Best Local Similarity 95.8%; Pred. No. 6.3e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DSWWTSLNFLGGTTVCLGQNSQSPSTNSHSPSCPTCPGYRWMLRRRIIFLFIILLCLLI 60
Db 32 DSWWTSLNFLGGTTVCLGQNSQSPSTNSHSPSCPTCPGYRWMLRRRIIFLFIILLCLLI 91
Qy 61 FLVLLDYQGILPVCPLIPGSSSTTSKGQCRTCTTPAQTSMYPSCCCTKPSDGNCTCPI 120
Db 92 FLVLLDYQGMPLVCPPLIPGSSSTTSKGQCRTCTTPAQTSMYPSCCCTKPSDGNCTCPI 151
Qy 121 PSSWAFGKFLWNASARFSLVLLVPFVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 180
Db 152 PSSWAFGKFLWNASARFSLVLLVPFVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 211
Qy 181 SPLLPPIFFC 189
Db 212 LPLLPPIFFC 220

RESULT 9

US-10-371-525-16
; Sequence 16, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13

; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-HBV-s
US-10-371-525-16

Query Match 95.9%; Score 1040; DB 15; Length 249;
Best Local Similarity 95.8%; Pred. No. 6.9e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DSWWTSLNFLGGTTVCLGQNSQSPSTNSHSPSCPTCPGYRWMLRRRIIFLFIILLCLLI 60
Db 56 DSWWTSLNFLGGTTVCLGQNSQSPSTNSHSPSCPTCPGYRWMLRRRIIFLFIILLCLLI 115
Qy 61 FLVLLDYQGILPVCPLIPGSSSTTSKGQCRTCTTPAQTSMYPSCCCTKPSDGNCTCPI 120
Db 116 FLVLLDYQGMPLVCPPLIPGSSSTTSKGQCRTCTTPAQTSMYPSCCCTKPSDGNCTCPI 175
Qy 121 PSSWAFGKFLWNASARFSLVLLVPFVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 180
Db 176 PSSWAFGKFLWNASARFSLVLLVPFVQWFGVLSPTVWLSVIMMMWYWGSPSLYSILSPF 235
Qy 181 SPLLPPIFFC 189
Db 236 LPLLPPIFFC 244

RESULT 10

US-10-371-069-16
; Sequence 16, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: Epimmune Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Cheenut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PADRE-HBV-s
US-10-371-069-16

Query Match 95.9%; Score 1040; DB 15; Length 249;
Best Local Similarity 95.8%; Pred. No. 6.9e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DSWWTSLNFLGGTTVCLGQNSQSPSTNSHSPSCPTCPGYRWMLRRRIIFLFIILLCLLI 60
Db 56 DSWWTSLNFLGGTTVCLGQNSQSPSTNSHSPSCPTCPGYRWMLRRRIIFLFIILLCLLI 115

Db 61 FLVLVDYQGIIPVCPILPGSSSTTSKGCRTCTTPAOGTSMYPSCCCTKPSDNCCTCIP1 120
116 FLVLVDYQGMIPVCPILPGSSSTTSKGCRTCTTPAOGTSMYPSCCCTKPSDNCCTCIP1 175
Qy 121 PSSWAFGKILMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMWYGPSSLYSILSPF 180
176 PSSWAFGKILMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMWYGPSSLYSILSPF 235
Qy 181 SPLPIFFC 189
Db 236 LPLPIFFC 244

RESULT 11
US-10-371-645-16
Sequence 16, Application US/10371645
Publication No. US20030216343A1
GENERAL INFORMATION:
APPLICANT: EpiMune Inc.
APPLICANT: Pikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Cheenut, Robert W.
APPLICANT: EpiMune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2002.11
CURRENT APPLICATION NUMBER: US/10/371,645
CURRENT FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PADRE-HBV-s
US-10-371-645-16

Query Match 95.9%; Score 1040; DB 15; Length 249;
Best Local Similarity 95.8%; Pred. No. 6.9e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DSWMTSLNPLGTTVCLGQNSQSPHSNHSPTSCPTCCGYRMCLRRPIIFILLCL1 60
Db 56 DSWMTSLNPLGTTVCLGQNSQSPHSNHSPTSCPTCCGYRMCLRRPIIFILLCL1 115
Qy 61 FLVLVDYQGIIPVCPILPGSSSTTSKGCRTCTTPAOGTSMYPSCCCTKPSDNCCTCIP1 120
Db 116 FLVLVDYQGMIPVCPILPGSSSTTSKGCRTCTTPAOGTSMYPSCCCTKPSDNCCTCIP1 175
Qy 121 PSSWAFGKILMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMWYGPSSLYSILSPF 180
Db 176 PSSWAFGKILMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMWYGPSSLYSILSPF 235
Qy 181 SPLPIFFC 189
Db 236 LPLPIFFC 244

RESULT 12
US-10-371-260-16
Sequence 16, Application US/10371260
Publication No. US20030220285A1
GENERAL INFORMATION:
APPLICANT: EpiMune Inc.
APPLICANT: Pikes, John D.

APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Cheenut, Robert W.
APPLICANT: EpiMune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-2002.13
CURRENT APPLICATION NUMBER: US/10/371,260
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: US 09/078,904
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 16
LENGTH: 249
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PADRE-HBV-s
US-10-371-260-16

Query Match 95.9%; Score 1040; DB 15; Length 249;
Best Local Similarity 95.8%; Pred. No. 6.9e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
Qy 1 DSWMTSLNPLGTTVCLGQNSQSPHSNHSPTSCPTCCGYRMCLRRPIIFILLCL1 60
Db 56 DSWMTSLNPLGTTVCLGQNSQSPHSNHSPTSCPTCCGYRMCLRRPIIFILLCL1 115
Qy 61 FLVLVDYQGIIPVCPILPGSSSTTSKGCRTCTTPAOGTSMYPSCCCTKPSDNCCTCIP1 120
Db 116 FLVLVDYQGMIPVCPILPGSSSTTSKGCRTCTTPAOGTSMYPSCCCTKPSDNCCTCIP1 175
Qy 121 PSSWAFGKILMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMWYGPSSLYSILSPF 180
Db 176 PSSWAFGKILMEWASARFWSLVLVPVQWFGVLSPTVWLSVIMMMWYGPSSLYSILSPF 235
Qy 181 SPLPIFFC 189
Db 236 LPLPIFFC 244

RESULT 13
US-09-247-890-12
Sequence 12, Application US/09247890
Publication No. US20020198162A1
GENERAL INFORMATION:
APPLICANT: Puumonen, Juha
APPLICANT: Bass, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen Library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/09/247,890
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: US 60/074,294
EARLIER FILING DATE: 1998-02-11
EARLIER APPLICATION NUMBER: US 60/105,509
EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 281
TYPE: PRT
ORGANISM: Hepatitis B virus
US-09-247-890-12

Mon Jul 25 17:03:30 2005

us-09-823-077c-7.rapb

Query Match 95.9%; Score 1040; DB 9; Length 281;
Best Local Similarity 95.8%; Pred. No. 7.8e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

1 DSWMTSLNFIAGTTTCVCLGNSQSPSTNSHPTSCPTCPGTRMCLRRFIIFILLICLI 60
88 DSWMTSLNFIAGTTTCVCLGNSQSPSTNSHPTSCPTCPGTRMCLRRFIIFILLICLI 147
61 FLVLLDYQGLIPVCPILPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDNCCTCIP 120
148 FLVLLDYQGLIPVCPILPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDNCCTCIP 207
121 PSSWAFGKYLMEWASARFWSLISLPVQWFGVLSPTVWLSVIMWMYWGPSLSYLSLSPF 180
208 PSSWAFGKYLMEWASARFWSLISLPVQWFGVLSPTVWLSVIMWMYWGPSLSYLSLSPF 267
181 SPLLPFFC 189
268 LPLLPFFC 276

RESULT 14
US-10-383-317-12
Sequence 12, Application US/10383317
Publication No. US2004001849A1
GENERAL INFORMATION:
APPLICANT: Punnonen, Juh
APPLICANT: Bass, Steven H.
APPLICANT: Whalen, Robert Gerald
APPLICANT: Howard, Russell
APPLICANT: Stemmer, Willem P.C.
APPLICANT: Maxygen, Inc.
TITLE OF INVENTION: Antigen library Immunization
FILE REFERENCE: 018097-028710US
CURRENT APPLICATION NUMBER: US/10/383,317
CURRENT FILING DATE: 2003-03-07
PRIOR APPLICATION NUMBER: US/09/247,890
PRIOR FILING DATE: 1999-02-10
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/074,294
PRIOR FILING DATE: EARLIER FILING DATE: 1998-02-11
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/105,509
PRIOR FILING DATE: EARLIER FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 281
TYPE: PRT
ORGANISM: Hepatitis B virus
US-10-383-317-12

Query Match 95.9%; Score 1040; DB 15; Length 281;
Best Local Similarity 95.8%; Pred. No. 7.8e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

1 DSWMTSLNFIAGTTTCVCLGNSQSPSTNSHPTSCPTCPGTRMCLRRFIIFILLICLI 60
88 DSWMTSLNFIAGTTTCVCLGNSQSPSTNSHPTSCPTCPGTRMCLRRFIIFILLICLI 147
61 FLVLLDYQGLIPVCPILPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDNCCTCIP 120
148 FLVLLDYQGLIPVCPILPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDNCCTCIP 207
121 PSSWAFGKYLMEWASARFWSLISLPVQWFGVLSPTVWLSVIMWMYWGPSLSYLSLSPF 180
208 PSSWAFGKYLMEWASARFWSLISLPVQWFGVLSPTVWLSVIMWMYWGPSLSYLSLSPF 267
181 SPLLPFFC 189
268 LPLLPFFC 276

Sequence 10, Application US/10472724
Publication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV B6 and E7 genes and proteins useful for vaccination
FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 334
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetic Construct
US-10-472-724-10

Query Match 95.9%; Score 1040; DB 16; Length 334;
Best Local Similarity 95.8%; Pred. No. 9.2e-82;
Matches 181; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

1 DSWMTSLNFIAGTTTCVCLGNSQSPSTNSHPTSCPTCPGTRMCLRRFIIFILLICLI 60
33 DSWMTSLNFIAGTTTCVCLGNSQSPSTNSHPTSCPTCPGTRMCLRRFIIFILLICLI 92
61 FLVLLDYQGLIPVCPILPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDNCCTCIP 120
93 FLVLLDYQGLIPVCPILPGSSSTTSKQCRCTCTPAQGTSMYPSCCCTKPSDNCCTCIP 152
121 PSSWAFGKYLMEWASARFWSLISLPVQWFGVLSPTVWLSVIMWMYWGPSLSYLSLSPF 180
153 PSSWAFGKYLMEWASARFWSLISLPVQWFGVLSPTVWLSVIMWMYWGPSLSYLSLSPF 212
181 SPLLPFFC 189
213 LPLLPFFC 221

Search completed: July 25, 2005, 11:38:01
Job time : 158 secs